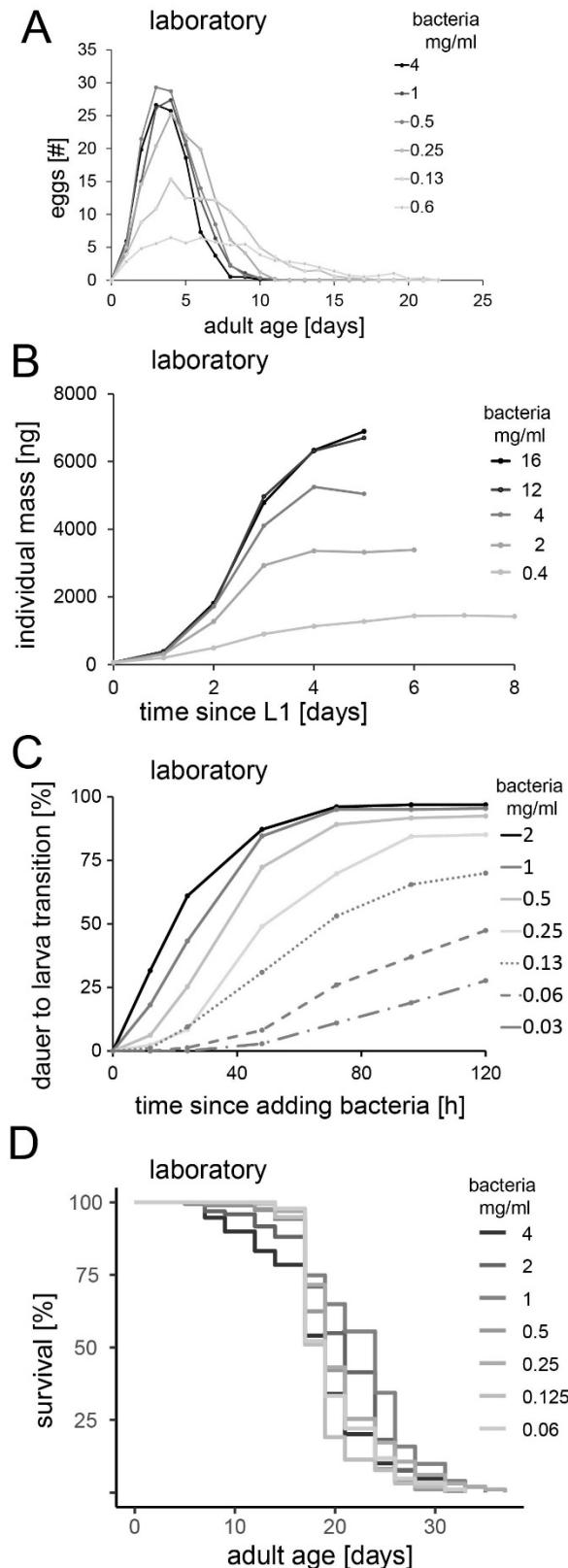
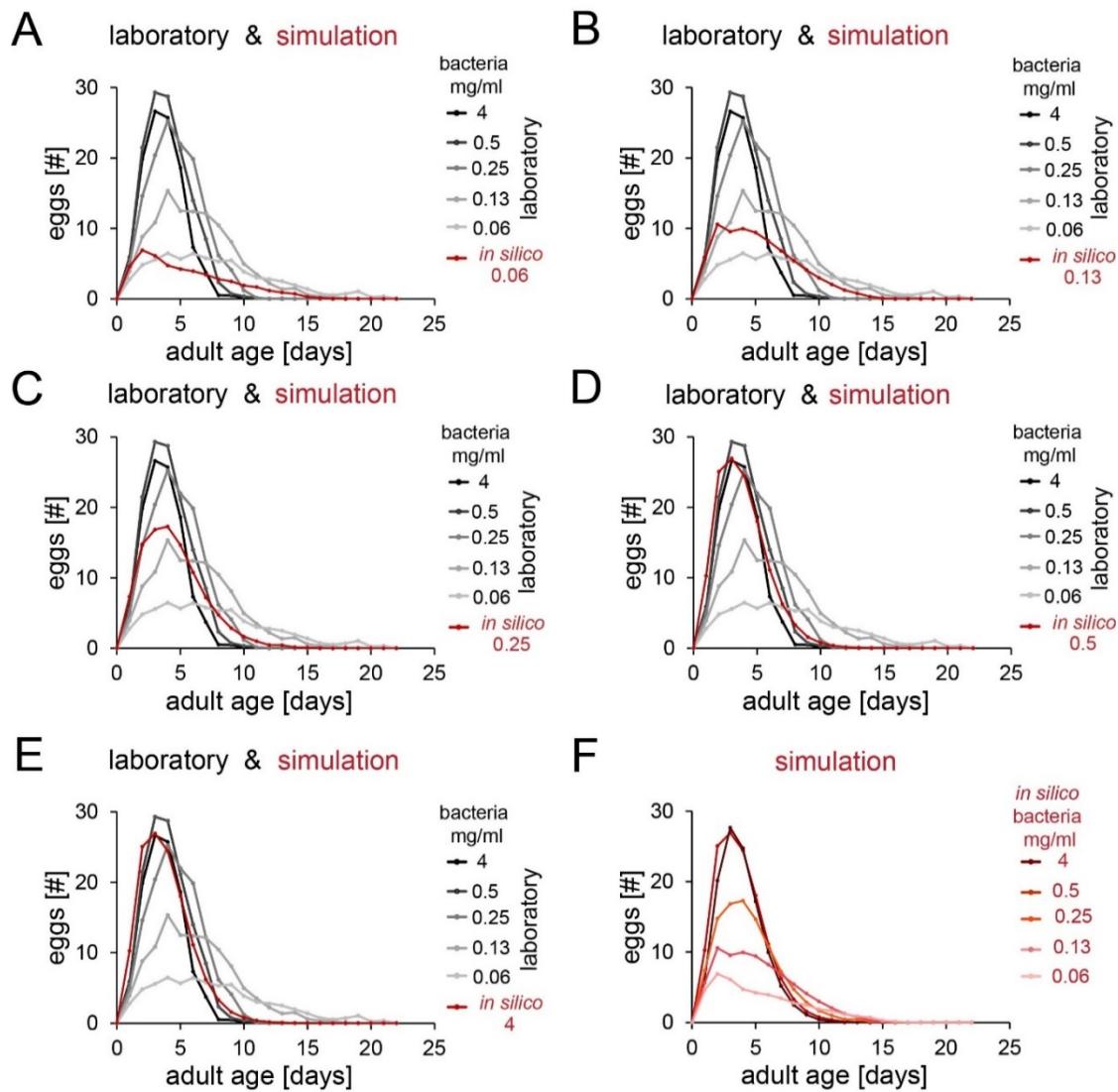


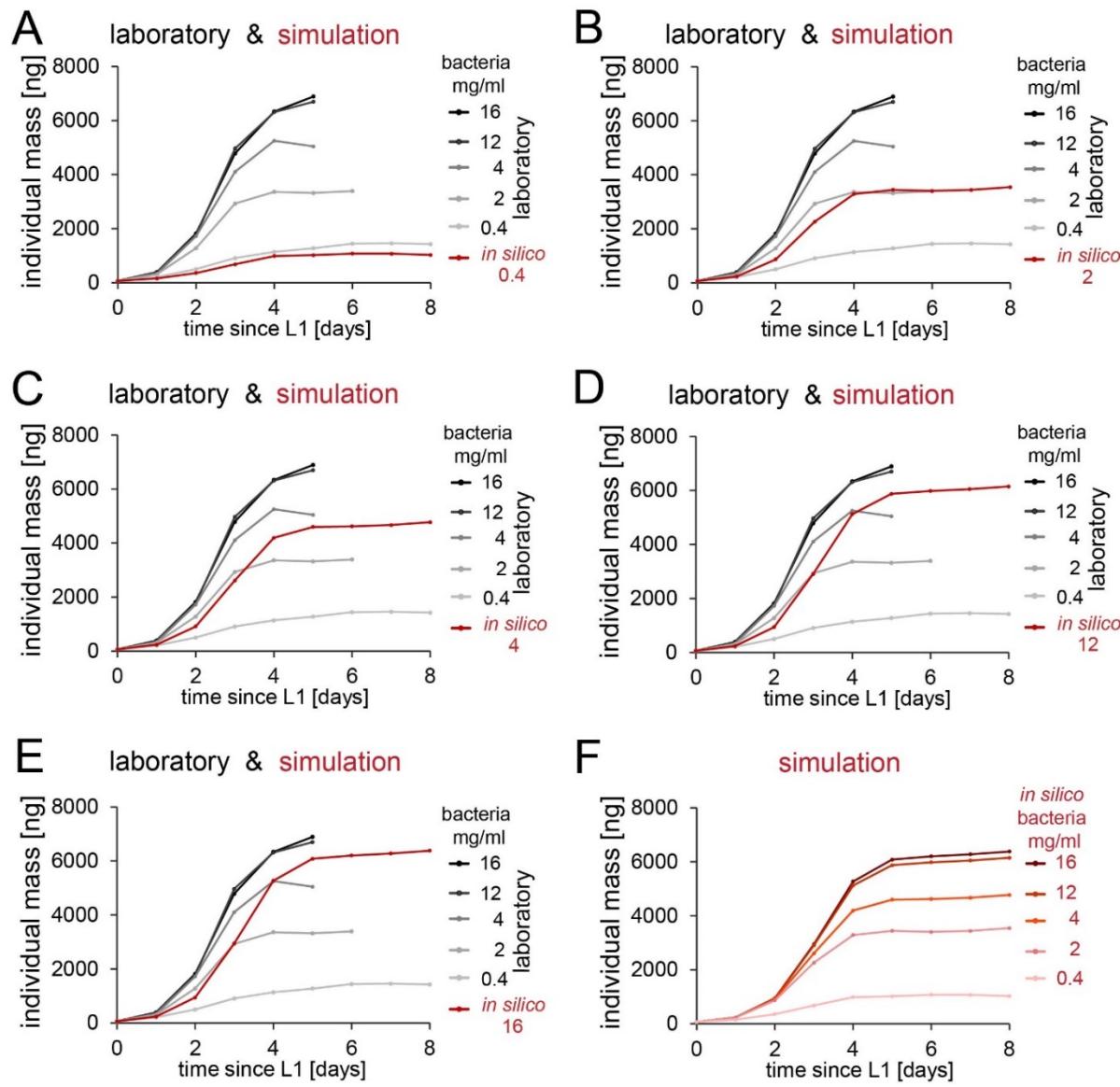
Supplementary Figure 1. Analysis of the laboratory population. The laboratory population was initialized with 5 mL of S-Medium, 250 *C. elegans* larvae, and 10 mg concentrated *E. coli* bacteria in a 50 mL plastic flask. Culling and feeding were performed every 24 or 48 hours. Culling provides a sample for analysis and is a form of extrinsic mortality; feeding restores the volume to 5 mL and provides a new supply of bacterial food. To determine the number of worms in the sample, we analyzed an aliquot of the 500 μ L cull sample using the COPAS biosort, an instrument designed for high throughput worm counting. As worms flow past a laser detection system, the instrument records time of flight, which is proportional to the length of the animal. The number of worms in the aliquot and the volume of the aliquot were used to calculate the total number of worms in the laboratory population, which can be plotted as a function of time to display population dynamics. To determine the concentration of bacteria in the laboratory population, we analyzed an aliquot of the 500 μ L cull sample using a spectrophotometer. The optical density with 600 nm light (OD600) is proportional to the number of bacteria. The OD600 values were converted to bacterial concentration using a standard curve and displayed on a graph.



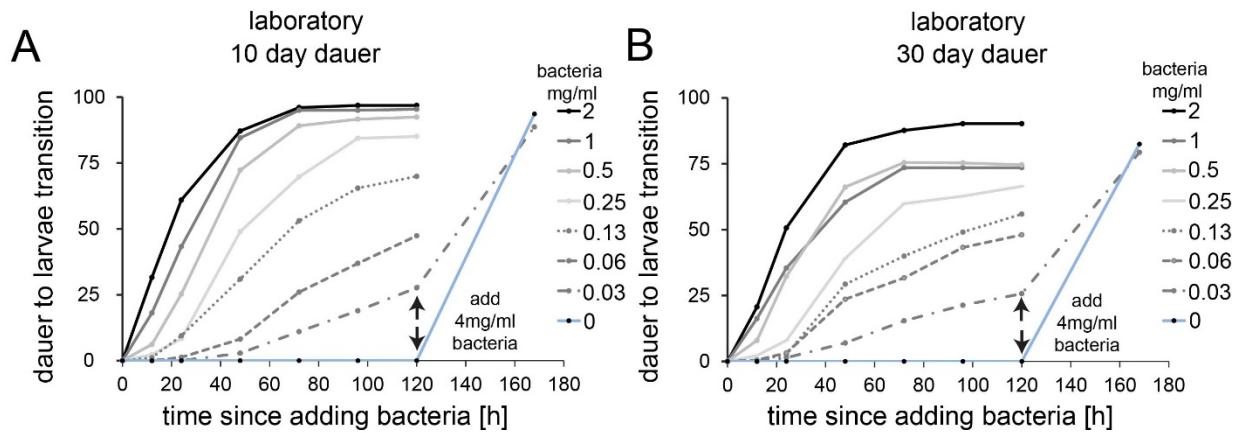
Supplementary Figure 2. Systematic analysis of laboratory worm properties. (A-D) Wild-type, self-fertile hermaphrodites were cultured in S-Medium with the indicated concentrations of *E. coli* (bacteria). (A) Daily progeny production of individual adults. The graph includes 2 additional data sets compared to Figure 2A. (B) Daily mass of individual larvae and adults. The graph includes 1 additional data set compared to Figure 2E. (C) A population of dauers were cultured with bacteria starting at time 0 - data shows average percent of larvae in the population. Animals were in the dauer stage for as many as 10 days. The graph includes 3 additional data sets compared to Figure 2I. (D) Representative survival curves for populations of individuals cultured with the bacterial concentration beginning at the L1 stage. The graph includes 3 additional data sets compared to Figure 2M. Lower concentrations of bacteria did not cause a substantial extension of adult lifespan, as might have been expected based on studies of caloric restriction. Notably, we initiated exposure to the bacterial concentration at the L1 stage and continued this same concentration throughout the adult life, whereas caloric restriction experiments often involve transferring young adults to the restricted food environment. N values and data are shown in Supplementary Tables 3-6a.



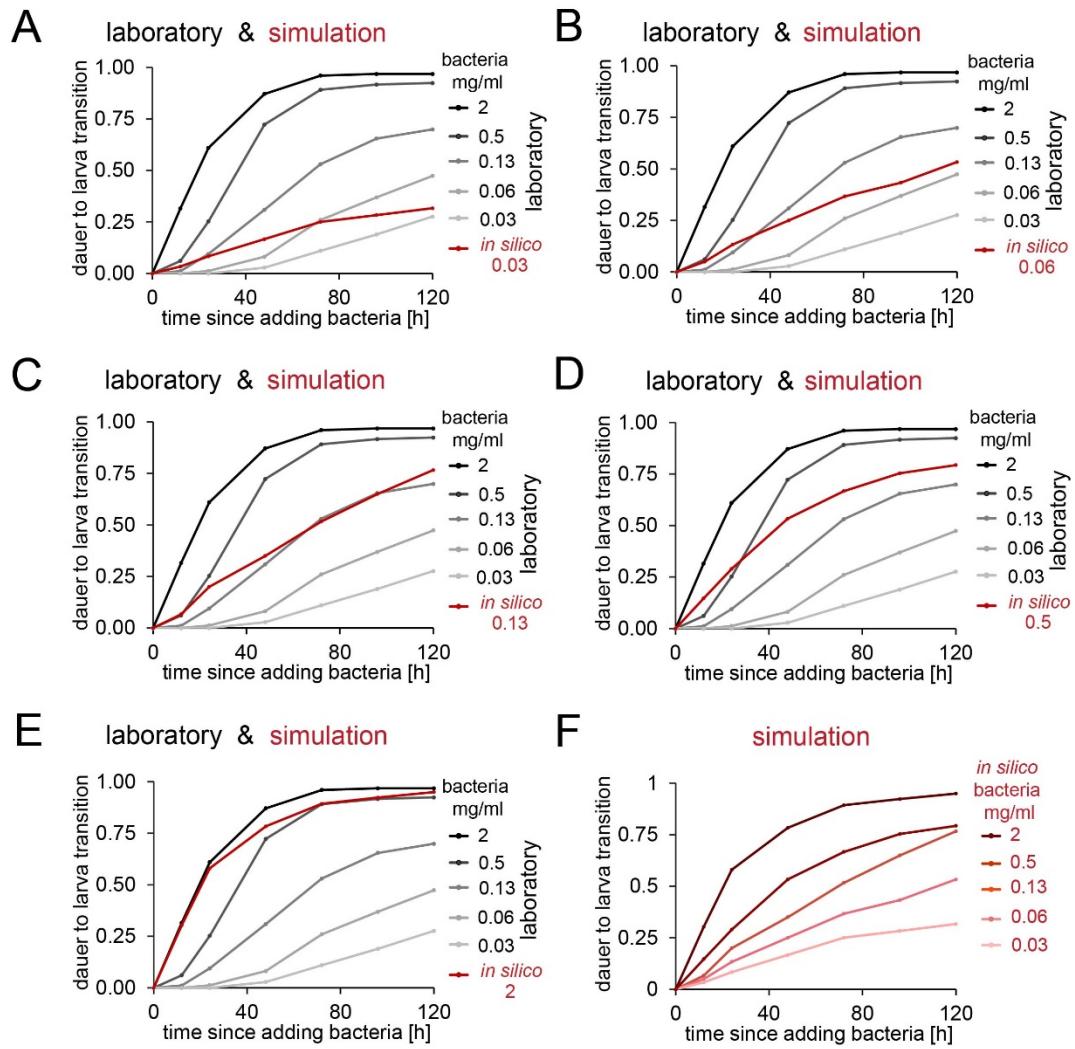
Supplementary Figure 3. Comparison of daily progeny production of laboratory and simulated worms. (A-E) Wild-type, self-fertile hermaphrodites were cultured in S-Medium with the indicated concentrations of *E. coli* (bacteria). Average daily progeny production of individuals is displayed as grey curves. The same data are displayed in Figure 2A,B, Supplementary Figure 2A, and Supplementary Table 3 (including N values). (A-F) The average daily progeny production of computationally simulated *in silico* worms in bacteria concentrations that correspond to the laboratory conditions is displayed as red curves. Panels A-E show that the single red curve corresponds well with the grey laboratory data with the same concentration of *E. coli*.



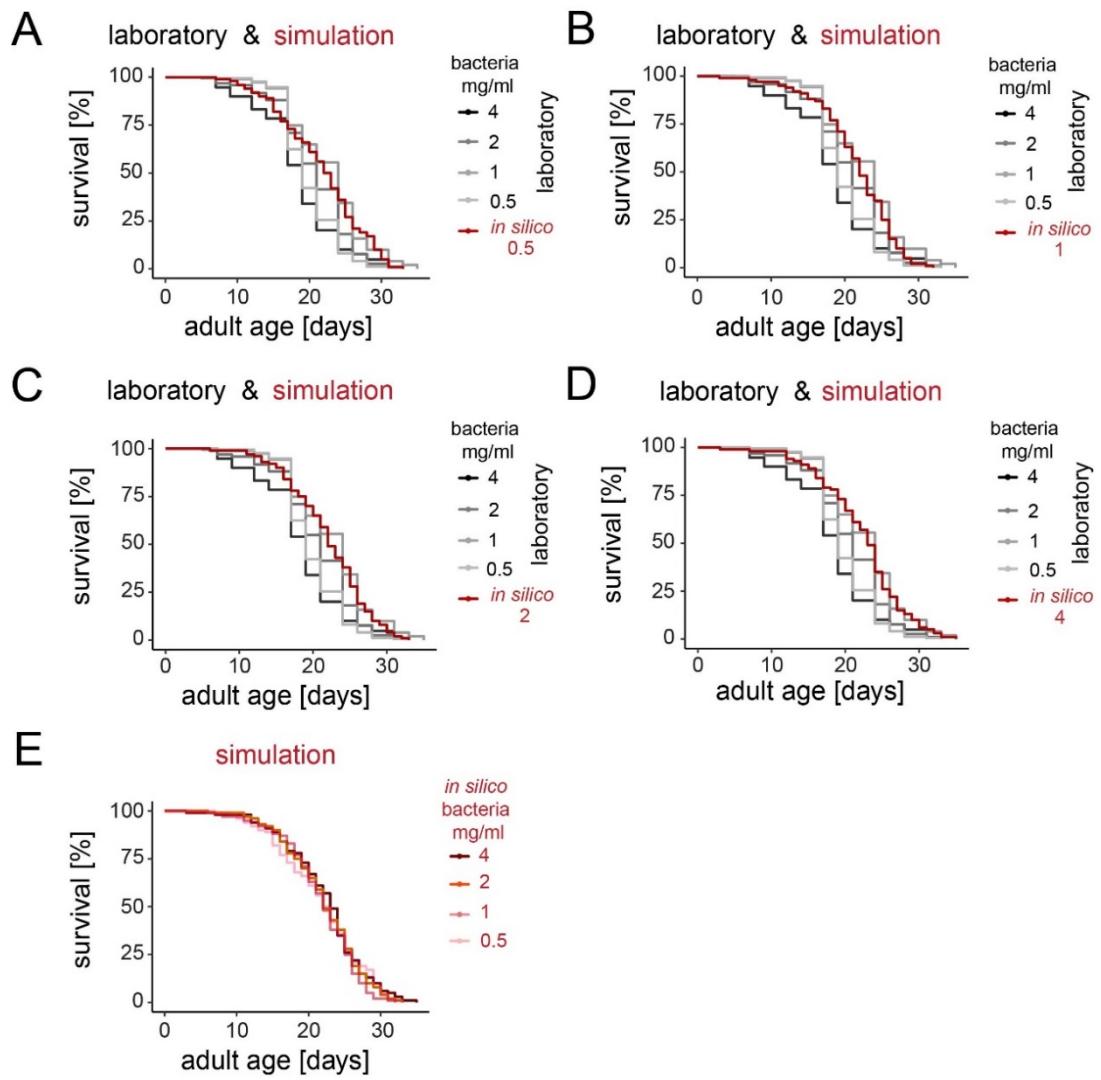
Supplementary Figure 4. Comparison of daily growth of laboratory and simulated worms.
 (A-E) Wild-type, self-fertile hermaphrodites were cultured in S-Medium with the indicated concentrations of *E. coli* (bacteria). Average daily mass of individuals is displayed as grey lines. The same data are displayed in Figure 2E,F, Supplementary Figure 2B, and Supplementary Table 4 (including N values). (A-F) The average daily mass of computationally simulated *in silico* worms in bacteria concentrations that correspond to the laboratory conditions is displayed as red lines. Panels A-E show that the single red line corresponds well with the grey laboratory data with the same concentration of *E. coli*.



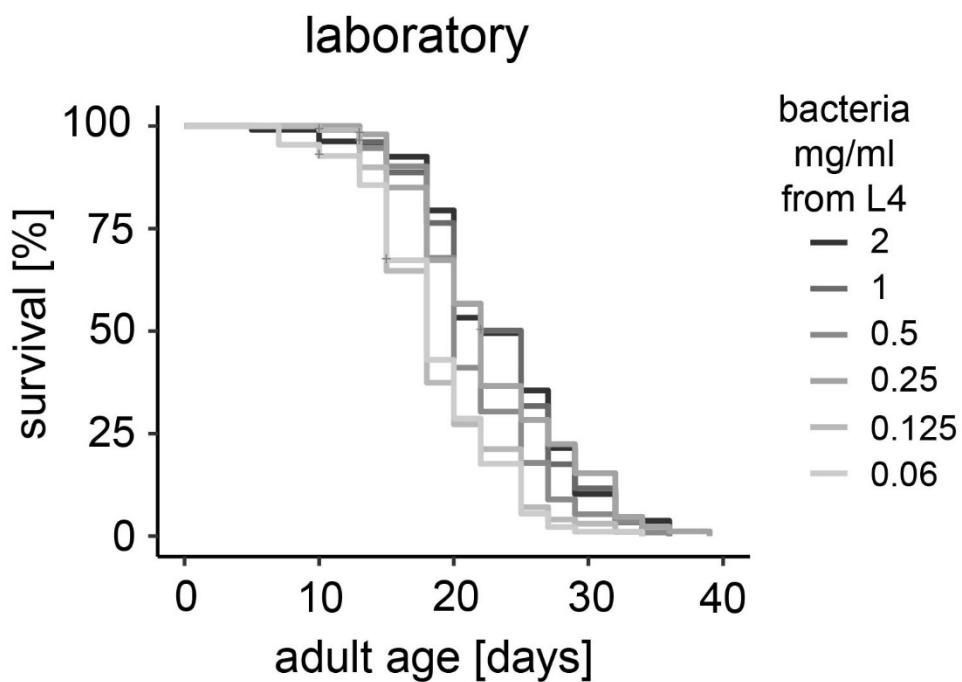
Supplementary Figure 5. Dauer to larva transition of 10-days old and 30-days old dauers in the laboratory. (A-B) A population of dauers were cultured with bacteria starting at time 0 - data shows average percent of larvae in the population. To determine the maximum potential to transition to larvae, we added 4 mg/mL bacteria after 120 hours to dauers that were cultured in 0 mg/mL and 0.03 mg/mL bacteria (black arrows indicate time of addition). The blue and dashed lines show dauer recovery at 170 hours (50 hours later) for dauers cultured in 0 mg/mL and 0.03 mg/mL bacteria, respectively. (A) Animals were in the dauer stage for as many as 10 days. Maximum transition percent at 120 hours was ~97%. The data in panel A are the same as Figure 2I,J, Supplementary Figure 2C, and Supplementary Table 5 (including N values). (B) Animals were in the dauer stage for as many as 30 days (1 month). Maximum transition percent at 120 hours was ~83%, indicating dauers gradually lose the ability to transition to larvae as they age.



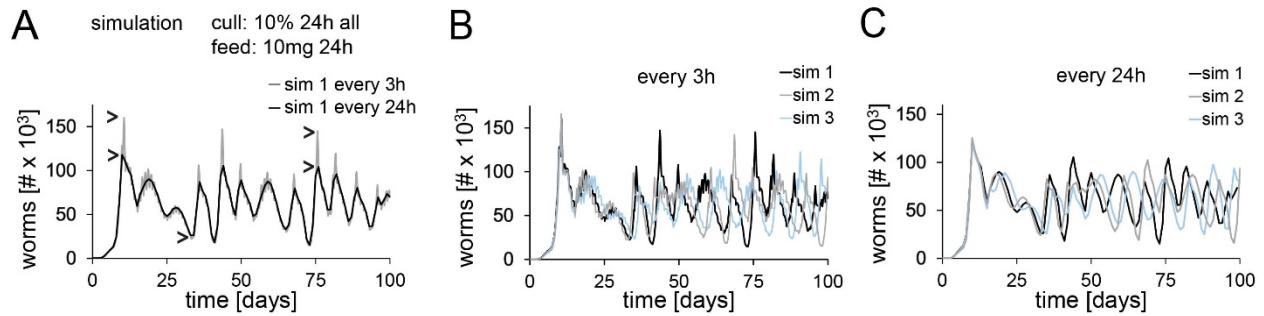
Supplementary Figure 6. Comparison of dauer to larva transition of laboratory and simulated worms. (A-E) A population of dauers were cultured with *E. coli* (bacteria) starting at time 0 – grey lines show average percent of larvae in the population. Animals were in the dauer stage for as many as 10 days. The same data are displayed in Figure 2I,J, Supplementary Figure 2C, and Supplementary Table 5 (including N values). (A-F) The average percent of larvae in the population of computationally simulated *in silico* worms in bacteria concentrations that correspond to the laboratory conditions is displayed as red lines. Panels A-E show that the single red line corresponds well with the grey laboratory data with the same concentration of *E. coli*.



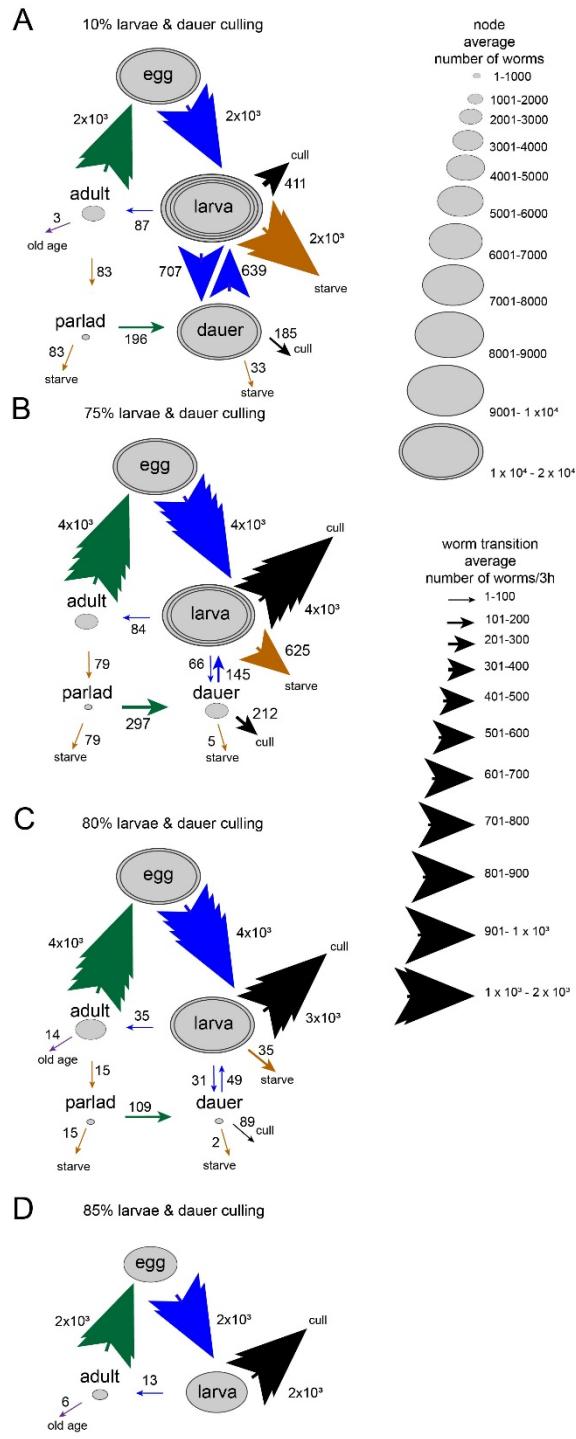
Supplementary Figure 7. Comparison of lifespans of laboratory and simulated worms. (A-D) Grey lines are representative survival curves for populations based on the analysis of individual wild-type hermaphrodites cultured with the bacterial concentration beginning at the L1 stage. The same data are displayed in Figure 2M,N, Supplementary Figure 2D, and Supplementary Table 6a (including N values). (A-E) Red lines are survival curves for populations based on the analysis of computationally simulated *in silico* worms in bacteria concentrations that correspond to the laboratory conditions. Panels A-E show that the bacteria concentration did not strongly affect the survival curves in the laboratory or the simulation.



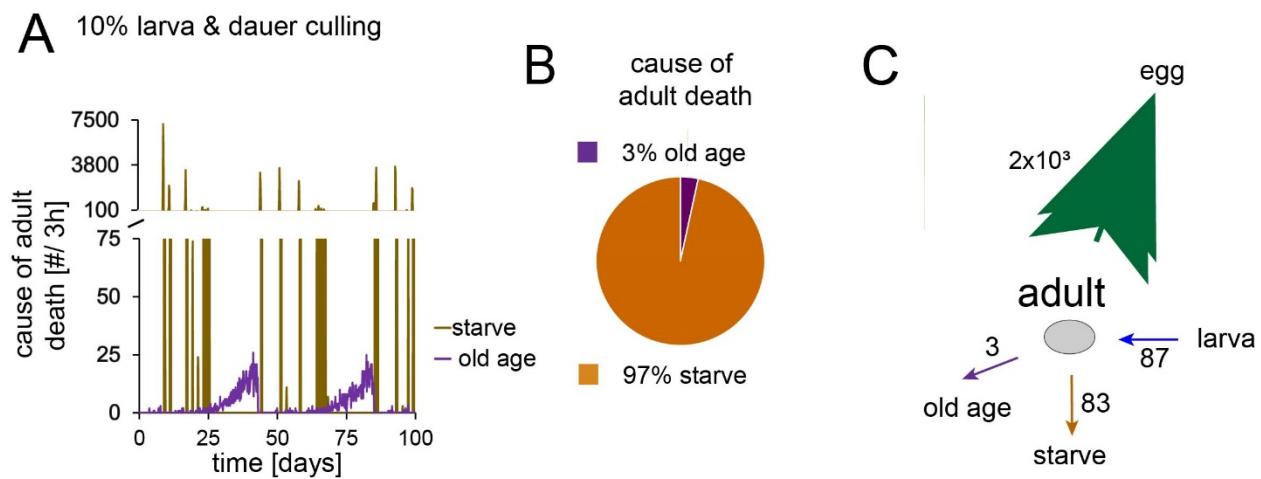
Supplementary Figure 8. Worms cultured in different food concentrations in the laboratory starting at the L4 larval stage displayed similar lifespans. Wild-type, self-fertile hermaphrodites were cultured in S-Medium with 2 mg/mL *E. coli*, shifted at the L4 larval stage to S-Medium with the indicated concentrations of *E. coli* bacteria, and monitored for survival. Representative survival curves are shown, and data are presented in Supplementary Table 6b (including N values).



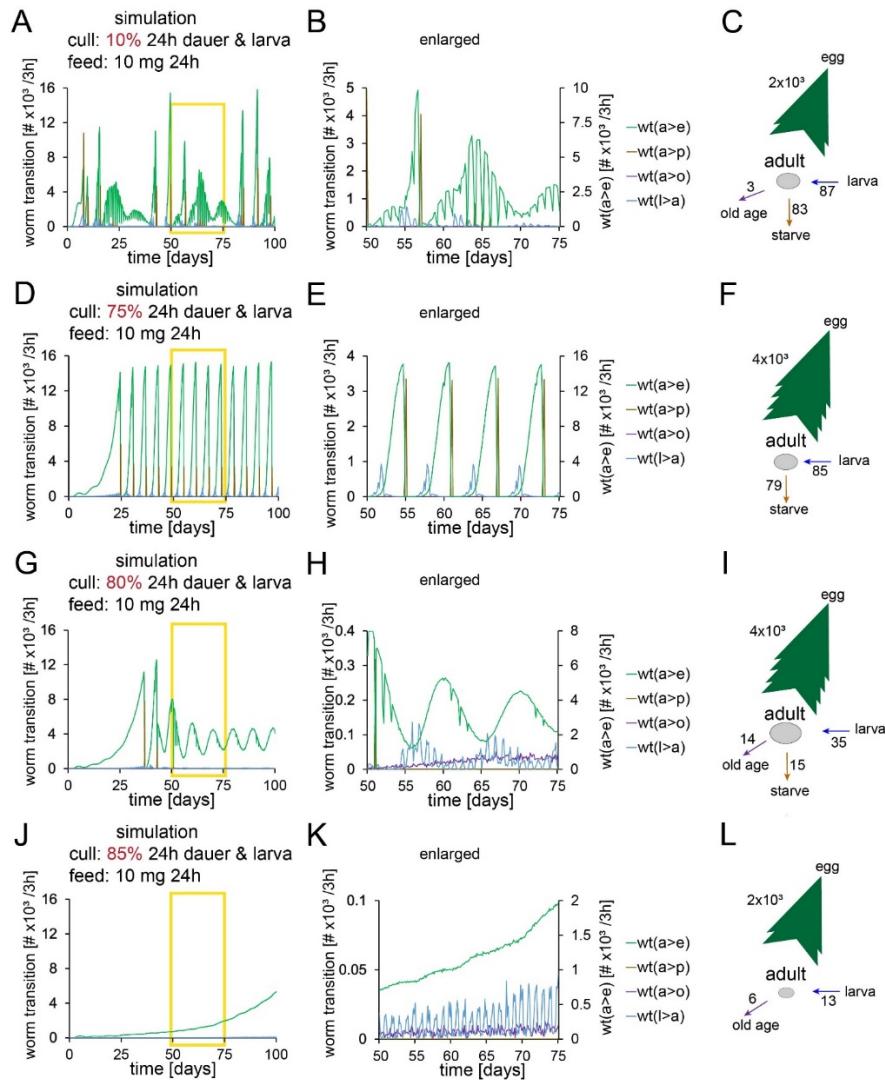
Supplementary Figure 9. Comparison of simulated data shown every 3 hours and every 24 hours. (A) The simulation uses 3-hour time steps, and thus it computes the number of worms 8 times/24 hours. By contrast, the laboratory population is analyzed once per day, and thus the number of worms is computed 1 time/24 hours. Therefore, it can be useful to plot the simulation data with 1 value/24 hours to compare with the laboratory population data. The graph shows the number of worms in the population with 1 value/24 h (black line) and 8 values/24h (grey line). When the data are plotted every three hours, the peaks are often higher and the valleys are often lower. Arrowheads indicate two peaks and one valley that illustrate these differences. The same data are shown in Figure 3B. (B, C) Three independently conducted simulations with the same parameters are displayed with 8 values/24h (every 3 hours) (B) and 1 value/24 (every 24 hours) (C). Panel C shows the same data as Figure 3B.



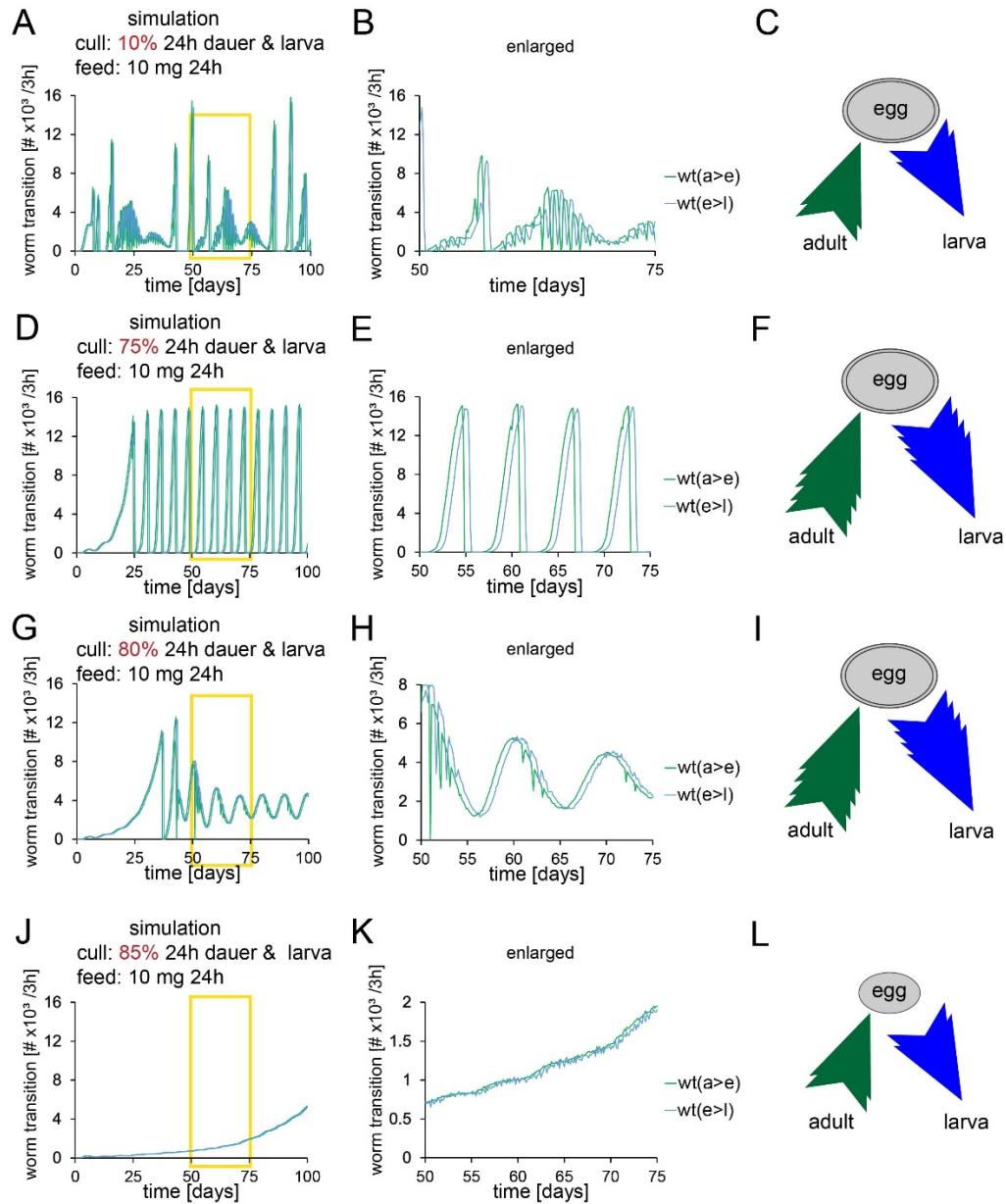
Supplementary Figure 10. Flow diagrams show larvae & dauer culling influence worm nodes and transitions. (A-D) Flow diagrams of simulated populations with 10 mg feeding and 10% (A), 75% (B), 80% (C), and 85% (D) stage-specific culling of dauers and larvae. The adult node of these diagrams is shown in Figure 5C, F, I. The scale bar shows how different node sizes in the flow diagram represent the different average number of worms in that node during the 100-day simulation. Similarly, the scale bar shows how different arrow sizes in the flow diagram represent different average number of worms making the transition during a 3-hour time period.



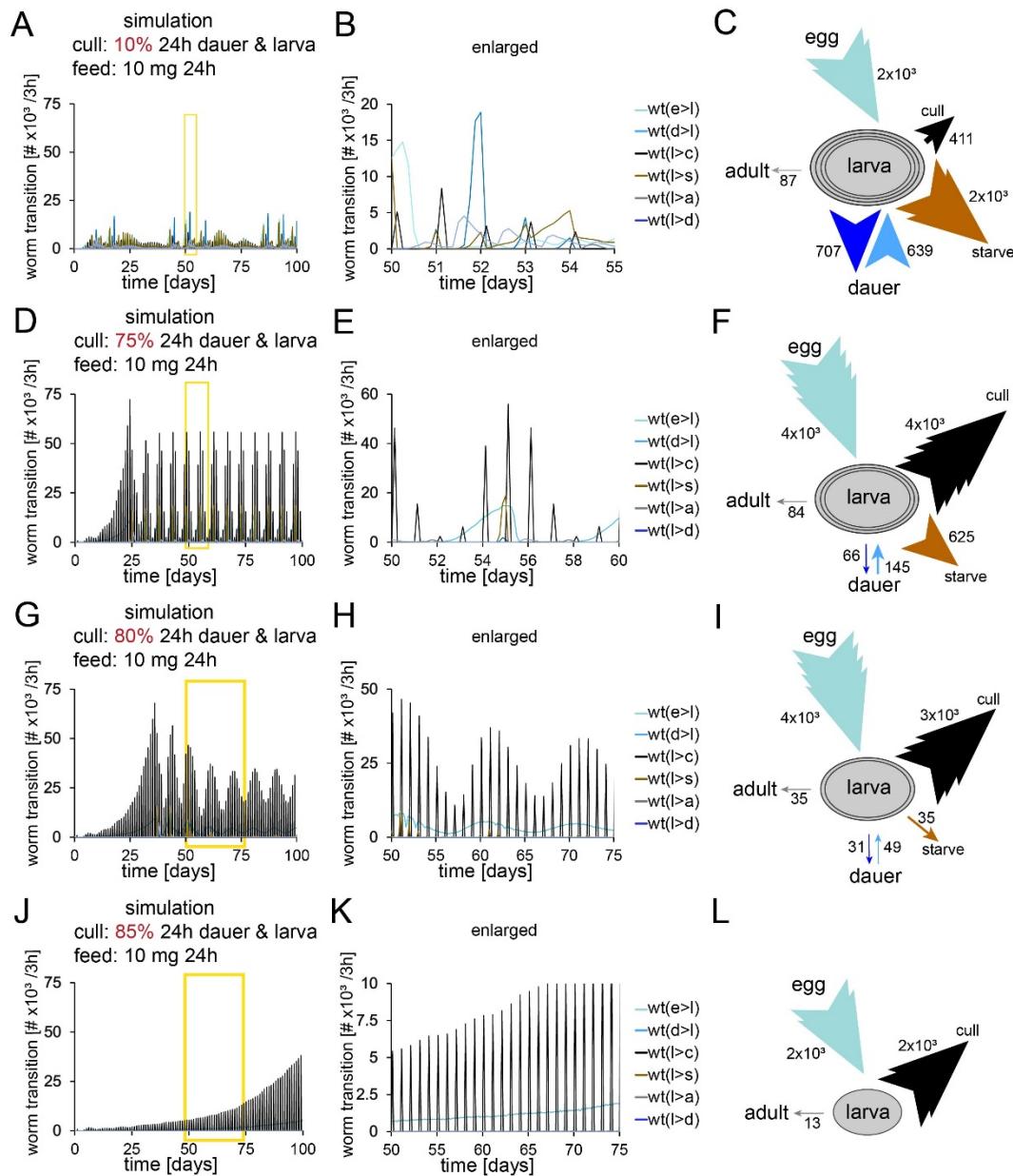
Supplementary Figure 11. Cause of adult death in simulated population with 10% larvae & dauer culling. (A) One representative simulated population with 10 mg feeding and 10% stage-specific culling of dauer and larvae is depicted. The death transitions of the adult node, starve ($wt(a>p)$) and old age ($wt(a>o)$), are displayed as number of worms/3 hours. (B) Pie chart displays the cause of adult death. (C) Flow diagram of the adult node displaying all worm transition rates.



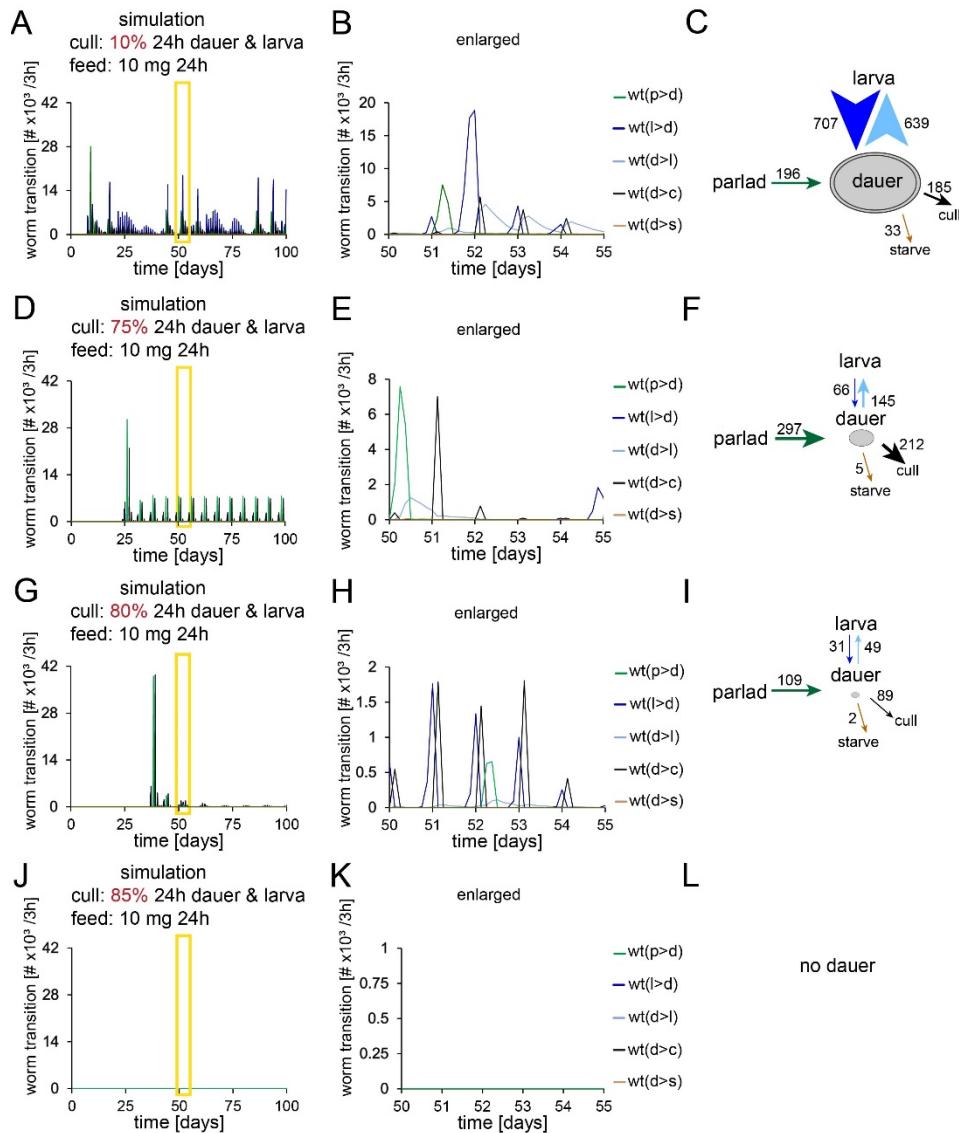
Supplementary Figure 12. Larva & dauer culling influences the worm transitions of the adult node. Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (G), and 85% (J) stage-specific culling of larva and dauer. The adult node is associated with five transitions: (1) $wt(l>a)$, (2) $wt(a>e)$, (3) $wt(a>p)$, (4) $wt(a>o)$, and (5) $wt(a>c)$. Because adult culling is set to zero as an input parameter in this computational simulation, $wt(a>c)$ is not shown. The transitions of the adult node are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-75, corresponding to the yellow boxes. The transition from adult to egg has a separate scale on the right, whereas the other three transitions use the scale on the left. (C,F,I,L) Flow diagrams of the adult node displaying all worm transition rates. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10–17.



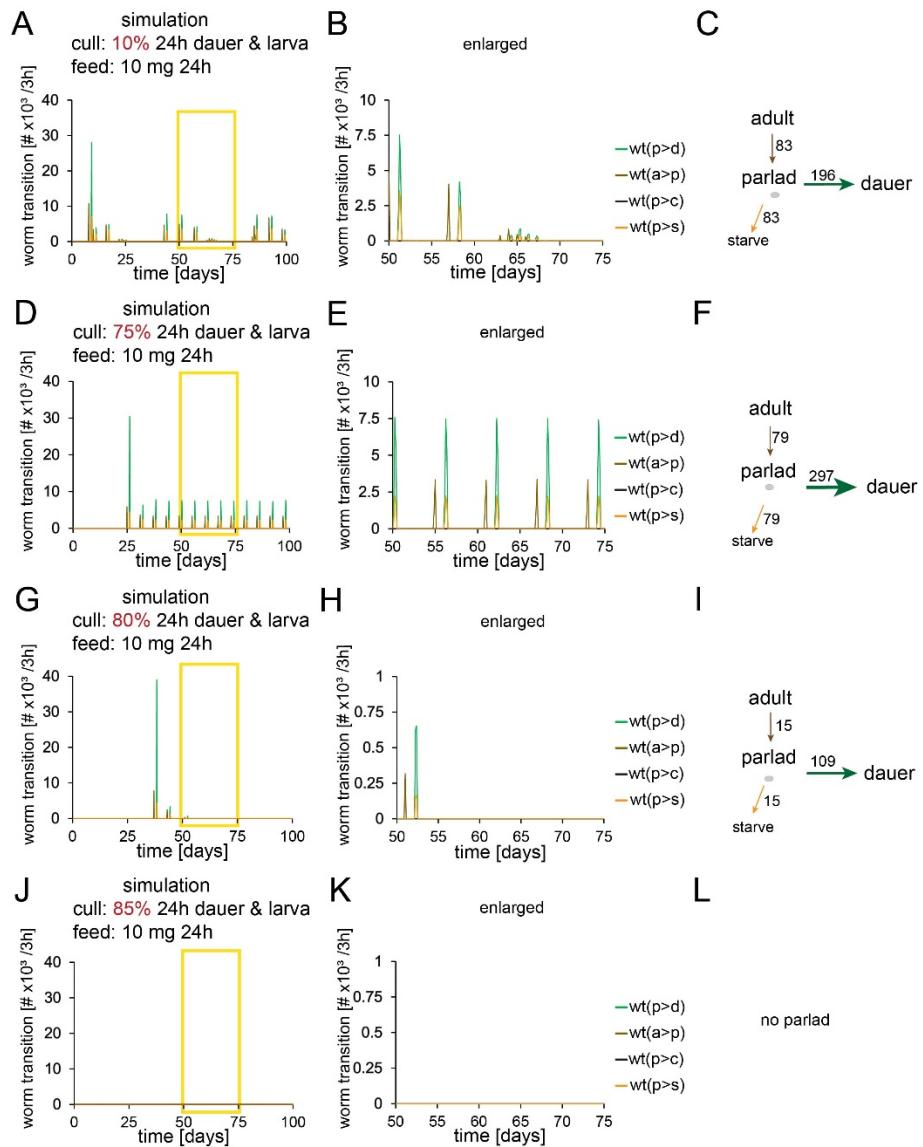
Supplementary Figure 13. Larva & dauer culling influences the worm transitions of the egg node. (A-D) Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (G), and 85% (J) stage-specific culling of larva and dauer. The egg node is associated with three transitions: (1) $wt(a>e)$, (2) $wt(e>l)$, and (3) $wt(e>c)$. Because egg culling is set to zero as an input parameter in this computational simulation, $wt(e>c)$ is not shown. The transitions of the egg node are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-75, corresponding to the yellow boxes. (C,F,I,L) Flow diagrams of the egg node displaying all worm transition rates. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10–17.



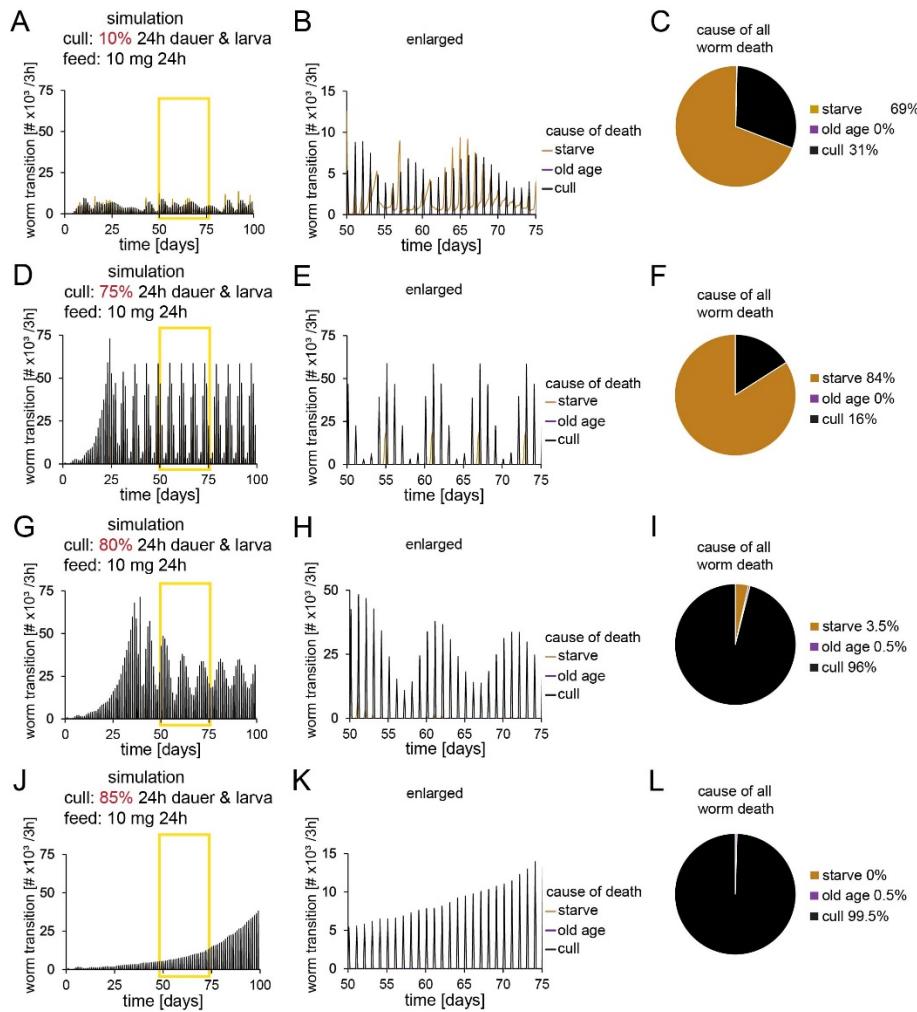
Supplementary Figure 14. Larva & dauer culling influences the worm transitions of the larva node. (A-D) Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (G), and 85% (J) stage-specific culling of larvae and dauer. The larva node is associated with six transitions: (1) $wt(e>l)$, (2) $wt(d>l)$, (3) $wt(l>a)$, (4) $wt(l>d)$, (5) $wt(l>c)$, and (6) $wt(l>s)$. The transitions of the larva node are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-75, corresponding to the yellow boxes. (C,F,I,L) Flow diagrams of the larva node displaying all worm transition rates. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10–17.



Supplementary Figure 15. Larva & dauer culling influences the worm transitions of the dauer node. (A-D) Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (H), and 85% (J) stage-specific culling of larva and dauer. The dauer node is associated with five transitions: (1) $wt(l>d)$, (2) $wt(p>d)$, (3) $wt(d>s)$, (4) $wt(d>l)$, and (5) $wt(d>c)$. The transitions of the dauer node are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-55, corresponding to the yellow boxes. (C,F,I,L) Flow diagrams of the dauer node displaying all worm transition rates. The simulated population with 85% stage-specific culling of larva and dauer does not contain any dauers. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10-17.



Supplementary Figure 16. Larva & dauer culling influences the worm transitions of the parlad node. (A-D) Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (G), and 85% (J) stage-specific culling of larva and dauer. The parlad node is associated with four transitions: (1) $wt(a>p)$, (2) $wt(p>d)$, (3) $wt(p>s)$, and (4) $wt(p>c)$. Because parlad culling is set to zero as an input parameter in this computational simulation, $wt(p>c)$ is not shown. The transitions of the parlad node are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-75, corresponding to the yellow boxes. (C,F,I,L) Flow diagrams of the parlad node displaying all worm transition rates. The simulated population with 85% stage-specific culling of larva and dauer does not contain any parlads. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10–17.



Supplementary Figure 17. Larva & dauer culling influences the cause of worm death. (A-D)

Representative simulated populations with 10 mg feeding and 10% (A), 75% (D), 80% (G), and 85% (J) stage-specific culling of larva and dauer (from 4, 6, 7, and 3 simulated populations). Starvation as a cause of death is associated with three transitions: (1) $wt(l>s)$, (2) $wt(d>s)$, and (3) $wt(p>s)$. In this Figure, starvation is the sum of these three transition rates. Culling as a cause of death is associated with five transitions: (1) $wt(a>c)$, (2) $wt(e>c)$, (3) $wt(l>c)$, (4) $wt(d>c)$, and (5) $wt(p>c)$. Because adult, egg, and parlad culling are set to zero as input parameters in this computational simulation, culling as a cause of death is the sum of $wt(l>c) + wt(d>c)$. Old age as a cause of death is associated with one transitions: (1) $wt(a>o)$. The transitions of the death nodes are displayed as number of worms/3 hours. (B,E,H,K) Enlargements show days 50-75, corresponding to the yellow boxes. (C,F,I,L) Pie charts display the cause of death for all worms. The same simulated populations are shown in Figure 4-5, Extended data Figure 5-6, and Supplementary Figure 10–16.

Supplemental Table 1. Summary statistics of the laboratory population with 10% culling and 10 mg *E. coli* feeding every 24 hours. Related to Figure 1B.

	replicate 1a	replicates 1a-c average of 3 +/- SD⁸
Initialize¹		
wt(i>l) ²	250	250
bt(i>b) ³ [ng]	10*10 ⁶	10*10 ⁶
Initialization Phase⁴		
Total time [days] ⁵	40	40 +/- 2
time to first peak [days] ⁶	29	29 +/- 2
Initialization & Maintenance Phase⁷		
average worm number	74 *10 ³	72 *10 ³ +/- 2*10 ³
max worm number	127 *10 ³	125 *10 ³ +/- 4*10 ³
total bacteria added [ng]	10*10 ⁸	10*10 ⁸
Maintenance Phase		
average worm number	81 *10 ³	79 *10 ³ +/- 3*10 ³
max worm number	112 *10 ³	111 *10 ³ +/- 1*10 ³
min worm number	58 *10 ³	57 *10 ³ +/- 2*10 ³

¹Initialize: starting amount of worms and bacteria for the experiment.

²wt(i>l), worm transition: initial addition of larvae.

³bt(i>b), bacteria transition, initial addition of bacteria.

⁴ Initialization Phase: defined in Figure 1B and Supplementary Section 1.

⁵Total time: duration of initialization phase.

⁶Time to first peak: defined in Figure 1B and Supplementary section 1.

⁷Maintenance Phase: defined in Figure 1B and Supplementary section 1.

⁸Values are from three biological replicates of the laboratory population conducted in parallel: replicates 1a-c. SD: Standard deviation.

Supplemental Table 2. Summary statistics of a single simulated worm.

Life events	Value / birth node / cause of death
¹ birth time	100. time step ² which time step was it born?
birth node	egg
³ cause of death	old age
death node	adult
⁴ egg span	5 time steps
⁴ larval span	20 time steps
⁴ dauer span	0 time steps
⁴ adult span	95 time steps
⁵ total reproductive span	54 time steps
⁶ total eggs	115
⁷ total mass eggs	7475 ng
⁸ total bacteria ingested	46125 ng
⁹ total cost of living	22303 ng

¹time-step when egg was laid or dauer burst out of parlad.

²The simulation begins at time step 1, and this animal was born at time step 100

³The three causes of death are starve, cull, and old age.

⁴Egg-, larval-, dauer-, adult span, number of time-steps the worm spent in egg, larva, dauer, and adult stage.

⁵Number of time-steps the worm generated eggs, from the first to the last egg.

⁶Total eggs, lifetime total of the number of eggs laid by the worm.

⁷Total mass eggs, lifetime total of egg mass laid by the worm – each egg is 65 ng.

⁸Total bacteria ingested, lifetime total of bacteria mass ingested by the worm ($bt(b>l) + bt(b>a)$).

⁹Total cost of living, lifetime total of mass used for metabolism by the worm. See Supplementary section 2-3.

Supplemental Table 3. Egg-laying summary statistics. Related to Figure 2A-D, Supplementary Figure 2A and 3.

lab ¹ /sim ²	bacteria concentration (mg/ml) ³	reproductive span to peak +/- SD (days) ⁴	reproductive span after peak +/- SD (days) ⁵	total reproductive span +/- SD (days) ⁶	peak progeny number +/- SD ⁷	total progeny number +/- SD ⁸	N ⁹ (n ¹⁰)
lab	4	3 +/- 1	7 +/- 2	10 +/- 1	27 +/- 5	109 +/- 19	4(80)
lab	1	4 +/- 1	6 +/- 2	10 +/- 1	27 +/- 2	116 +/- 10	3(58)
lab	0.5	3 +/- 1	6 +/- 2	10 +/- 5	29 +/- 4	132 +/- 16	4(73)
lab	0.25	5 +/- 1	7 +/- 1	11 +/- 1	25 +/- 2	131 +/- 22	4(75)
lab	0.13	5 +/- 1	11 +/- 1	16 +/- 2	15 +/- 3	109 +/- 18	4(88)
lab	0.06	4 +/- 2	14 +/- 1	18 +/- 3	6 +/- 2	67 +/- 15	4(91)
sim	4	3 +/- 0	11 +/- 1	14 +/- 1	28 +/- 0.2	115 +/- 0.2	3(300)
sim	1	3 +/- 0	11 +/- 1	14 +/- 1	28 +/- 0	116 +/- 0.1	3(300)
sim	0.5	3 +/- 0	13 +/- 2	16 +/- 2	27 +/- 0	128 +/- 0.1	3(300)
sim	0.25	4 +/- 0	14 +/- 0	18 +/- 0	17 +/- 0	100 +/- 0.1	3(300)
sim	0.13	4 +/- 0	14 +/- 2	18 +/- 2	11 +/- 0.1	77 +/- 0.3	3(300)
sim	0.06	4 +/- 0	14 +/- 2	18 +/- 2	7 +/- 0.1	46 +/- 0.2	3(300)

Values are mean with standard deviation (SD).

¹lab: data from laboratory experiments.

²sim: data from computational simulations.

³bacteria concentration: concentration of bacteria in the laboratory experiment or the simulation – held constant in these experiments and simulations.

⁴reproductive span to peak: time from adult day 0 until day of peak egg laying (Figure 2C).

⁵reproductive span after peak: time from day of peak egg laying until last day of egg laying (Figure 2C).

⁶total reproductive span: time from adult day 0 until last day of egg laying (Figure 2C).

⁷peak progeny number: Number of eggs laid on day of peak progeny production (Figure 2C).

⁸total progeny number: Total number of eggs laid (Figure 2C).

⁹N: Number of independent laboratory experiments or simulations.

¹⁰n: Number of worms analyzed.

Supplemental Table 4. Growth summary statistics. Related to Figure 2E-H, Supplementary Figure 2B and 4.

lab ¹ / sim ²	bacteria concentration (mg/ml) ³	Sexual maturity growth span (days) ⁴	Maximum size +/- SD (ng) ⁵	sexual maturity size (ng) ⁶	Maximum size growth span (days) ⁷	N ⁸ (n ⁹)
lab	16	2.5	6900 +/-300	nd	5	4(38- 166)
lab	12	2.5	6700 +/-500	3600	5	4(42- 166)
lab	4	2.5	5300 +/-600	3000	5	4(54- 166)
lab	2	2.5	3400 +/-300	2800	6	4(58- 166)
lab	0.4	2.5	1400 +/-100	1800	6	4(41- 166)
sim	16	3	6400 +/-1	2900 +/-0	8	3(300)
sim	12	3	6100 +/-2	2900 +/-0	8	3(300)
sim	4	3	4800 +/-1	2600 +/- 0.5	8	3(300)
sim	2	3	3400 +/-2	2300 +/- 0	6	3(300)
sim	0.4	4	1100 +/-2	1000 +/-3	6	3(300)

Values are mean with standard deviation (SD).

¹lab: data from cross sectional laboratory experiments.

²sim: data from computational simulations.

³bacteria concentration: concentration of bacteria in the laboratory experiment or the simulation – held constant in these experiments and simulations.

⁴sexual maturity growth span: time from L1 until the time of sexual maturity (Figure 2G).

⁵maximum size: largest mass of a hermaphrodite (Figure 2G).

⁶sexual maturity size: mass when the eggs can first be observed inside the hermaphrodite (Figure 2G) N2(n19,25,25,17).

⁷maximum size growth span: time from L1 until the time of largest mass of a hermaphrodite (Figure 2G).

⁸N: Number of independent laboratory experiments or simulations.

⁹n: Number of worms analyzed.

Supplemental Table 5. Dauer to larva transition summary statistics. Related to Figure 2I-L, Supplementary Figure 2C, 5, and 6.

lab ¹ /sim ²	bacteria concentration (mg/ml) ³	Transition span 50% (hours) ⁴	Transition percent at 120 hours +/- SD ⁶	N ⁷ (n ⁸)
lab	2	12-24	97 +/- 2	4(316)
lab	1	24- 48	95 +/- 3	4(320)
lab	0.5	24- 48	92 +/- 3	4(319)
lab	0.25	48-72	85 +/- 10	4(299)
lab	0.13	48-72	70 +/- 13	4(281)
lab	0.06	not reached ⁵	47 +/- 20	4(346)
lab	0.03	not reached ⁵	28 +/- 22	4(317)
lab	0	not reached ⁵	0	4(311)
sim	5	0-12	97 +/- 1	3(300)
sim	2	12-24	95 +/- 1	3(300)
sim	0.5	24-48	79 +/- 7	3(300)
sim	0.13	48-72	77 +/- 10	6(60)
sim	0.06	96-120	53 +/- 16	6(60)
sim	0.03	not reached ⁵	32 +/- 13	6(60)

Values are mean with standard deviation (SD).

¹lab: data from laboratory experiments.

²sim: data from computational simulations.

³bacteria concentration: concentration of bacteria in the laboratory experiment or the simulation – held constant in these experiments and simulations.

⁴transition span 50%: time from adding bacteria until 50% of dauers transition to larva (Figure 2K).

⁵not reached: less than 50% of dauers transitioned to larvae after 120 hours.

⁶transition percent at 120 hours: percent of dauers that transitioned to larvae after 120 hours (Figure 2K).

⁷N: Number of independent laboratory experiments or simulations.

⁸n: Number of worms analyzed.

Supplemental Table 6a. Lifespan summary statistics – transition at L1 stage. Related to Figure 2M-O, Supplementary Figure 2D and 7.

lab ¹ /si m ²	Bacteria concentration (mg/ml) ³	Mean adult lifespan +/- SD (days) ⁴	Maximum adult lifespan (days) ⁵	N ⁶ (n ⁷)
lab L1	4	18	30	2(374)
lab L1	2	20	30	2(367)
lab L1	1	21	34	2(325)
lab L1	0.5	20	31	2(343)
sim L1	4	22	35	1(100)
sim L1	2	22	33	1(100)
sim L1	1	22	32	1(100)
sim L1	0.5	22	33	1(100)

Values are mean with standard deviation (SD).

¹lab: data from laboratory experiments.

²sim: data from computational simulations.

³bacteria concentration: concentration of bacteria in the laboratory experiment or the simulation – held constant in these experiments and simulations.

⁴mean adult lifespan: average adult lifespan (Figure 2O).

⁵maximum adult lifespan: lifespan of the longest lived worm (Figure 2O).

⁶N: Number of independent laboratory experiments or simulations.

⁷n: Number of worms analyzed.

Supplemental Table 6b. Lifespan summary statistics – transition at L4 stage. Related to Supplementary Figure 8.

lab ¹	Bacteria concentration (mg/ml) ²	Mean adult lifespan +/- SD (days) ³	Maximum adult lifespan (days) ⁴	N ⁵ (n ⁶)
lab L4	2	18	32	2(266)
lab L4	1	18	27	2(248)
lab L4	0.5	17	28	2(246)
lab L4	0.25	18	29	2(223)
lab L4	0.13	16	27	2(227)
lab L4	0.06	16	27	2(203)

Values are mean with standard deviation (SD).

¹lab: data from laboratory experiments.

²bacteria concentration: concentration of bacteria in the laboratory experiment – held constant in these experiments and simulations.

³mean adult lifespan: average adult lifespan (Figure 2O).

⁴maximum adult lifespan: lifespan of the longest lived worm (Figure 2O).

⁵N: Number of independent laboratory experiments or simulations.

⁶n: Number of worms analyzed.

Supplemental Table 7. Summary statistics of *C. elegans* laboratory population and corresponding simulation. Displayed in Figure 3, Extended Data Figure 2, 3, 4, Supplementary Figure 9.

system	feedin g / culling frequ ency (hours)	culling perce nt	feeding amount [mg bacteri a]	Time to first peak [days] ¹	average worm number x10 ³ (initializati on & maintenance phase) ^{2,3}	averag e worm numbe r x10 ³ (maint enanc e phase) ³	Maximum worm number x10 ³ (initializati on & maintenan ce phase) ^{2,3}	maximu m worm number x10 ³ (mainten ance phase) ³	minimu m worm number x10 ³ (mainte nance phase) ³
laboratory	24	10	10	26 +/-0	36 +/-2	32 +/-2	120 +/-12	71 +/-8	3 +/-2
laboratory	24	10	5	25 +/-1	15 +/-2	14 +/-3	70 +/-28	70 +/-28	0.8 +/-0.4
laboratory	24	5	5	27 +/-1	29 +/-4	23 +/-5	138 +/-27	67 +/-4	2 +/-1.6
laboratory	48	10	10	28 +/-1	26 +/-4	21 +/-5	72 +/-9	53 +/-17	5 +/-0.9
<i>in silico</i>	24	10	10	10 +/-0	59 +/-1	62 +/-2	122 +/-6	104 +/-5	21 +/-5
<i>in silico</i>	24	10	5	10 +/-1	34 +/-2	36 +/-2	64 +/-4	67 +/-9	8 +/-2
<i>in silico</i>	24	5	5	11 +/-0	37 +/-6	38 +/-0	67 +/-0.2	63 +/-2	11 +/-5
<i>in silico</i>	48	10	10	9 +/-0	24 +/-0.5	25 +/-0.5	68 +/-1	59 +/-2	9 +/-0.1

Values are averages of three independent experiments +/- Standard Deviation.

¹ Time to first peak: duration of time to first peak, defined in Figure 1B and Supplementary section 1.

² Initialization Phase: defined in Figure 1B and Supplementary section 1.

³ Maintenance Phase: defined in Figure 1B and Supplementary section 1.

Supplemental Table 8. The effects of dauer & larva culling on population dynamics when maximum adult lifespan is 40 days. Displayed in Figure 4A-E, 5.

larva and dauer culling [%] ¹	average worm number (x10 ³) ²	average egg fraction [%] ³	average adult fraction [%] ³	average larva fraction [%] ³	average dauer fraction [%] ³	average parlad fraction [%] ³	<u>Cause of adult death (%)⁴</u>
0	66 +/-1	14 +/-0	3 +/-0	58 +/-0	24 +/-1	1 +/-0	90 +/-3 10 +/-3
10	61 +/-1	16 +/-0	3 +/-0	60 +/-0	19 +/-0	1 +/-0	97 +/-1 3 +/-1
20	58 +/-1	20 +/-0	4 +/-0	61 +/-0	14 +/-0	1 +/-0	96 +/-2 4 +/-2
30	58 +/-1	23 +/-0	4 +/-0	61 +/-0	11 +/-0	2 +/-0	99 +/-0 1 +/-0
40	56 +/-4	26 +/-2	4 +/-0	59 +/-0	8 +/-1	3 +/-1	100 +/-0 0 +/-0
50	50 +/-0	27 +/-0	6 +/-0	55 +/-0	8 +/-0	4 +/-0	100 +/-0 0 +/-0
60	51 +/-1	32 +/-0	6 +/-0	52 +/-1	6 +/-0	4 +/-0	100 +/-0 0 +/-0
70	48 +/-2	35 +/-1	6 +/-1	51 +/-1	5 +/-1	2 +/-1	93 +/-11 7 +/-11
75	48 +/-2	39 +/-0	6 +/-2	50 +/-0	3 +/-1	1 +/-1	83 +/-25 17 +/-25
77	44 +/-1	39 +/-0	8 +/-2	50 +/-0	2 +/-1	1 +/-0	58 +/-19 42 +/-19
80	39 +/-0	40 +/-0	9 +/-0	49 +/-0	2 +/-0	0 +/-0	49 +/-5 51 +/-5
82.5	34 +/-0	41 +/-0	9 +/-0	48 +/-0	2 +/-0	0 +/-0	53 +/-2 47 +/-2
84	29 +/-0	41 +/-0	9 +/-1	48 +/-0	2 +/-0	0 +/-0	59 +/-13 41 +/-13
84.5	26 +/-1	41 +/-0	8 +/-1	48 +/-0	2 +/-1	0 +/-0	61 +/-13 39 +/-14
85	13 +/-2	43 +/-0	10 +/-0	48 +/-0	0 +/-0	0 +/-0	100 +/-0

Values are averages with standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases +/- Standard Deviation.

¹larva and dauer culling: percentage of all larvae and dauers culled every 24 hours.

Supplementary section that egg, adult and parlad stages were not culled.

²average worm number: value includes all five worm stages.

³average egg/adult/larva/dauer/parlad fraction: average percentage of eggs/adults/larva/dauer/parlad in the population.

⁴cause of adult death: Adults can die of (1) starvation, (2) old age, or (3) culling. Since adult culling is a user-programmable input that was set to 0, all adults die of old age or starvation.

Supplemental Table 9. The effects of egg culling on population dynamics with maximum adult lifespan of 40 days. Displayed in Figure 4G-H.

egg culling [%] ¹	average worm number (x10 ³) ²	average egg fraction [%] ³	average adult fraction [%] ³	average larva fraction [%] ³	average dauer fraction [%] ³	average parlad fraction [%] ³	Cause of adult death (%) ⁴
0	65 +/-2	14 +/-0	3 +/-0	58 +/-1	24 +/-1	1 +/-0	92 +/-4 8 +/-4
20	56 +/-0	14 +/-0	4 +/-0	50 +/-0	28 +/-0	3 +/-0	100 +/-0 0 +/-0
40	49 +/-1	20 +/-2	7 +/-1	44 +/-1	25 +/-3	4 +/-1	97 +/-7 3 +/-7
60	44 +/-0	19 +/-0	9 +/-0	35 +/-0	28 +/-0	8 +/-0	100 +/-0 0 +/-0
80	35 +/-3	26 +/-9	14 +/-3	27 +/-3	26 +/-5	8 +/-3	98 +/-3 2 +/-3
82	32 +/-3	30 +/-10	16 +/-3	24 +/-4	23 +/-6	7 +/-3	97 +/-3 3 +/-3
83	29 +/-2	36 +/-8	18 +/-2	21 +/-3	20 +/-5	5 +/-3	94 +/-3 6 +/-3
84	26 +/-0	41 +/-0	21 +/-0	19 +/-0	16 +/-0	3 +/-0	90 +/-1 10 +/-1
85	16 +/-0	52 +/-0	40 +/-0	9 +/-0	0 +/-0	0 +/-0	0 +/-0 100 +/-0
90	1 +/-0	50 +/-0	44 +/-0	5 +/-0	0 +/-0	0 +/-0	0 +/- 100 +/-0

Values are averages with standard deviation from 10 independent simulations and represent the entire simulation, including the initialization and maintenance phases +/- Standard Deviation.

¹egg culling: percentage all eggs culled every 6 hours. Supplementary section that dauer, larva, adult and parlad stages were not culled.

²average worm number: value includes all five worm stages.

³average egg/adult/larva/dauer/parlad fraction: average percentage of eggs/adults/larva/dauer/parlad in the population.

⁴cause of adult death: Adults can die of (1) starvation, (2) old age, or (3) culling. Since adult culling is a user-programmable input that was set to 0, all adults die of old age or starvation.

Supplemental Table 10. The effects of dauer & larva culling on dauer mutant population dynamics with maximum adult lifespan of 40 days. Displayed in Figure 4I-J.

larva and dauer culling [%] ¹	average worm number (x10 ³) ²	average egg fraction [%] ³	average adult fraction [%] ³	average larva fraction [%] ³	average dauer fraction [%] ³	average parlad fraction [%] ³	<u>Cause of adult death (%)⁴</u>
							starve old age
0	58 +/- 6	16 +/- 1	4 +/- 0	76 +/- 2	1 +/- 1	2 +/- 1	96 +/- 4 4 +/- 4
20	64 +/- 0	23 +/- 0	8 +/- 0	63 +/- 0	2 +/- 0	4 +/- 0	100 +/- 0 0 +/- 0
40	58 +/- 1	26 +/- 0	8 +/- 0	65 +/- 0	1 +/- 0	1 +/- 0	70 +/- 4 30 +/- 4
60	52 +/- 1	32 +/- 0	9 +/- 0	58 +/- 0	0 +/- 0	0 +/- 0	50 +/- 9 50 +/- 9
80	38 +/- 0	40 +/- 0	10 +/- 0	50 +/- 0	0 +/- 0	0 +/- 0	16 +/- 3 84 +/- 3
85	17 +/- 5	43 +/- 0	10 +/- 0	48 +/- 0	0 +/- 0	0 +/- 0	0 +/- 0 100 +/- 0

Values are averages with standard deviation from 10 independent simulations and represent the entire simulation, including the initialization and maintenance phases +/- Standard Deviation.

¹larva and dauer culling: percentage of all larvae and dauers culled every 24 hours. Egg, adult and parlad stages were not culled.

²average worm number: value includes all five worm stages.

³average egg/adult/larva/dauer/parlad fraction: average percentage of eggs/adults/larva/dauer/parlad in the population.

⁴cause of adult death: Adults can die of (1) starvation, (2) old age, or (3) culling. Since adult culling is a user-programmable input that was set to 0, all adults die of old age or starvation.

Supplemental Table 11. The effects of dauer & larva culling on population dynamics when maximum adult lifespan is 25 days. Displayed in Figure 6A-B.

larva and dauer culling [%] ¹	average worm number ($\times 10^3$) ²	average egg fraction [%] ³	average adult fraction [%] ³	Cause of adult death (%) ⁴	
				starve	old age
0	67 +/-1	14 +/-0	3 +/-0	91 +/-0	9 +/-0
10	65 +/-4	15 +/-2	3 +/-1	91 +/-2	9 +/-2
20	59 +/-1	20 +/-0	4 +/-0	93 +/-1	7 +/-1
30	58 +/-1	23 +/-0	4 +/-0	95 +/-3	5 +/-3
40	56 +/-4	26 +/-2	4 +/-0	100 +/-0	0 +/-0
50	51 +/-1	27 +/-1	6 +/-0	99 +/-1	1 +/-1
60	51 +/-0	33 +/-0	6 +/-0	100 +/-0	0 +/-0
70	50 +/-1	36 +/-0	6 +/-0	94 +/-4	6 +/-4
75	49 +/-0	39 +/-0	5 +/-0	98 +/-0	2 +/-0
76	47 +/-1	39 +/-0	5 +/-0	98 +/-0	2 +/-0
77	48 +/-1	40 +/-0	7 +/-0	43 +/-6	57 +/-6
80	43 +/-0	41 +/-0	7 +/-0	36 +/-2	64 +/-2
82.5	37 +/-0	42 +/-0	7 +/-0	38 +/-1	62 +/-1
84	31 +/-0	42 +/-0	7 +/-0	44 +/-1	56 +/-1
84.5	27 +/-2	43 +/-1	7 +/-0	48 +/-1	52 +/-1
85	18 +/-4	44 +/-0	7 +/-0	0 +/-0	100 +/-0

Values are averages standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases.

¹larva and dauer culling: percentage of all larvae and dauers culled every 24 hours. Egg, adult and parlad stages were not culled.

²average worm number: value includes all five worm stages.

³average egg/adult fraction: average percentage of eggs/adults in the population.

⁴cause of adult death: Adults can die of (1) starvation, (2) old age, or (3) culling. Since adult culling is a user-programmable input that was set to 0, all adults die of old age or starvation.

Supplemental Table 12. The effects of dauer & larva culling on population dynamics when maximum adult lifespan is 60 days. Displayed in Figure 6A-B.

larva and dauer culling [%] ¹	average worm number ($\times 10^3$) ²	average egg fraction [%] ³	average adult fraction [%] ³	Cause of adult death (%) ⁴	
				starve	old age
0	68 +/-0	14 +/-0	4 +/-0	95 +/-0	5 +/-0
10	62 +/-0	16 +/-0	4 +/-0	99 +/-0	1 +/-0
20	57 +/-1	19 +/-0	5 +/-0	98 +/-0	2 +/-0
30	57 +/-1	23 +/-1	5 +/-0	98 +/-1	2 +/-1
40	54 +/-1	25 +/-0	6 +/-0	97 +/-0	3 +/-0
50	52 +/-3	28 +/-1	6 +/-1	96 +/-6	4 +/-6
60	51 +/-1	33 +/-0	6 +/-0	100 +/-0	0 +/-0
70	48 +/-1	36 +/-0	8 +/-1	94 +/-3	6 +/-3
75	49 +/-0	39 +/-0	5 +/-0	100 +/-0	0 +/-0
76	48 +/-0	40 +/-0	5 +/-0	100 +/-0	0 +/-0
77	40 +/-0	38 +/-0	11 +/-1	64 +/-7	36 +/-7
80	37 +/-0	39 +/-0	11 +/-0	60 +/-6	40 +/-6
82.5	32 +/-0	40 +/-0	11 +/-0	64 +/-1	36 +/-1
84	28 +/-1	40 +/-0	10 +/-0	82 +/-1	18 +/-1
84.5	24 +/-2	40 +/-0	9 +/-1	79 +/-1	21 +/-1
85	19 +/-5	41 +/-1	11 +/-0	49 +/-35	51 +/-35
85.5	9 +/-4	42 +/-0	12 +/-0	0 +/-0	100 +/-0

Values are averages with standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases.

¹larva and dauer culling: percentage of all larvae and dauers culled every 24 hours. Egg, adult and paralad stages were not culled.

²average worm number: value includes all five worm stages.

³average egg/adult fraction: average percentage of eggs/adults in the population.

⁴cause of adult death: Adults can die of (1) starvation, (2) old age, or (3) culling. Since adult culling is a user-programmable input that was set to 0, all adults die of old age or starvation.

Supplemental Table 13. The effects of adult culling on population dynamics when maximum adult lifespan is 40 days and dauer & larva culling is 80%. Displayed in Figure 6E.

larva and dauer culling [%] ¹	adult culling [%] ²	averag e worm number ($\times 10^3$) ³	average egg fraction [%] ⁴	average adult fraction [%] ⁴	Cause of adult death (%) ⁵		
					cull	starve	old age
80	0	39 +/-0	40 +/-0	9 +/-0	0 +/-0	49 +/-5	51 +/-5
80	5	39 +/-1	41 +/-0	7 +/-0	53 +/-4	28 +/-7	19 +/-3
80	10	35 +/-6	41 +/-0	6 +/-0	70 +/-1	24 +/-1	6 +/-0
80	15	23 +/-2	42 +/-1	6 +/-0	90 +/-12	7 +/-13	3 +/-0
80	20	2 +/-1	42 +/-0	5 +/-0	98 +/-0	0 +/-0	2 +/-0
80	25	0.4 +/-0	41 +/-0	5 +/-0	99 +/-0	0 +/-0	1 +/-0
80	30	0.3 +/-0	39 +/-0	5 +/-0	99 +/-0	0 +/-0	1 +/-0

Values are averages with standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases.

¹larva and dauer culling: 80 percent of all larvae and dauers were culled every 24 hours. Egg and parlad stages were never culled.

²adult culling: percent of adults culled every 24 hours.

³average worm number: value includes all five worm stages.

⁴average egg/adult fraction: average percentage of eggs/adults in the population.

⁵cause of adult death: Adults can die of (1) culling, (2) starvation, or (3) old age.

Supplemental Table 14. The effects of adult culling on population dynamics when maximum adult lifespan is 25 days and dauer & larva culling is 77%. Displayed in Figure 6D.

larva and dauer culling [%] ¹	adult culling [%] ²	averag e worm number ($\times 10^3$) ³	average egg fraction [%] ⁴	average adult fraction [%] ⁴	cull	<u>Cause of adult death (%)⁵</u>	
						starve	old age
77	0	48 +/-1	40 +/-0	7 +/-0	0 +/-0	43 +/-6	57 +/-6
77	5	46 +/-0	40 +/-0	6 +/-0	41 +/-0	25 +/-0	34 +/-0
77	10	44 +/-0	40 +/-0	5 +/-0	63 +/-1	20 +/-1	17 +/-0
77	15	41 +/-1	41 +/-0	5 +/-0	78 +/-3	12 +/-4	10 +/-1
77	20	33 +/-0	41 +/-0	5 +/-0	81 +/-1	14 +/-1	5 +/-0
77	25	11 +/-3	41 +/-0	5 +/-0	97 +/-0	0 +/-0	3 +/-0
77	30	0.2 +/-0	40 +/-0	5 +/-0	98 +/-0	0 +/-0	2 +/-0
77	35	0.2 +/-0	38 +/-1	5 +/-0	99 +/-1	0 +/-0	1 +/-1
77	40	0.3 +/-0	36 +/-1	5 +/-0	99 +/-1	0 +/-0	1 +/-1

Values are averages with standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases.

¹larva and dauer culling: 77 percent of all larvae and dauers were culled every 24 hours. Egg and parlad stages were never culled.

²adult culling: percent of adults culled every 24 hours.

³average worm number: value includes all five worm stages.

⁴average egg/adult fraction: average percentage of eggs/adults in the population.

⁵cause of adult death: Adults can die of (1) culling, (2) starvation, or (3) old age.

Supplemental Table 15. The effects of adult culling on population dynamics when maximum adult lifespan is 60 days and dauer & larva culling is 85%. Displayed in Figure 6F.

larva and dauer culling [%] ¹	adult culling [%] ²	averag e worm number (x10 ³) ³	average egg fraction [%] ⁴	average adult fraction [%] ⁴	cull	Cause of adult death (%) ⁵		
						starve	old age	
85	0	19 +/-5	41 +/-1	11 +/-0	0 +/-0	49 +/-35	51 +/-35	
85	5	3 +/-1	42 +/-0	9 +/-0	83 +/-1	0 +/-0	17 +/-1	
85	10	0.5 +/-0.2	42 +/-0	7 +/-0	96 +/-1	0 +/-0	4 +/-1	
85	15	0.3 +/-0.06	40 +/-1	6 +/-0	98 +/-1	0 +/-0	2 +/-1	
85	20	0.2 +/-0.06	39 +/-1	5 +/-0	100 +/-0	0 +/-0	0 +/-0	

Values are averages with standard deviation from at least three independent simulations and represent the entire simulation, including the initialization and maintenance phases.

¹larva and dauer culling: 85 percent of all larvae and dauers were culled every 24 hours. Egg and parlad stages were never culled.

²adult culling: percent of adults culled every 24 hours.

³average worm number: value includes all five worm stages.

⁴average egg/adult fraction: average percentage of eggs/adults in the population.

⁵cause of adult death: Adults can die of (1) culling, (2) starvation, or (3) old age.

Supplementary Section 1: Description of the laboratory population

Development of a simple laboratory system with two species, *C. elegans* and *E. coli*:

Complex ecosystems with many species and dynamic environments captivate the imagination: the Serengeti plain of Africa with its spectacular migrations, or the Amazon rainforest with its numerous species interacting in intricate food webs^{4,5}. While the complexity of these systems is part of their appeal, it also presents challenges for experimental analysis and understanding. As an alternative approach to address fundamental questions about the function of ecosystems, we employed reductionist logic by conceiving of the simplest possible ecosystem. We reasoned that even the simplest ecosystem would embody basic principles of population dynamics that are relevant to complex ecosystems. Furthermore, a simple ecosystem offers powerful experimental advantages, since it can be analyzed, manipulated, and modeled. This logic leads to a question: what are the essential features of an ecosystem that must be included in a simple laboratory system? The formal definition of an ecosystem is that it is the unit of a community of organisms and their non living environment⁶. All ecosystems occupy a finite amount of space⁷. A simple ecosystem would have a small volume – this is quantitatively different from the vast Serengeti, but not qualitatively different. All ecosystems have a flux of nutrients to support organismal life⁸. A simple ecosystem would have a controlled influx of nutrients - this is different from a complex ecosystem based on sunlight that is converted to chemical energy by photosynthesis leading to trophic pyramids, but not qualitatively different. A simple ecosystem would have two species capable of indefinite reproduction - this is quantitatively different from the Amazon rainforest with thousands of species, but not qualitatively different⁶. Every species in the Amazon displays population dynamics: fluctuations in the size and age distribution of its populations. We propose that understanding the basic principles of population dynamics in a simple ecosystem will be relevant to complex ecosystems where the population dynamics of multiple species play out in parallel over time.

To generate such a simple ecosystem, we constructed an environment consisting of a plastic vial with 5 mL of water containing simple salts. To provide essential nutrients, we periodically added *E. coli* bacteria, the first species in the system. The *E. coli* do not replicate because the solution does not contain a carbon source to support bacterial cell division, and their controlled influx can be considered as migration. The replicating and main species in this environment is *Caenorhabditis elegans*, a terrestrial nematode. *C. elegans* is a good choice for this simple ecosystem for several reasons: (1) *C. elegans* is an important model organism for studies of basic biological processes, and there is a wealth of information about its genetics and biology. Procedures for measuring individual traits are well established, and this facilitates the creation of realistic models. (2) It has two sexual forms: self-fertile hermaphrodites and males. In liquid culture systems, essentially all animals are hermaphrodites, because males do not mate effectively in these conditions. A population of self-fertile hermaphrodites simplifies the analysis and modeling. (3) *C. elegans* has a rapid life cycle and a short adult lifespan –it develops from an egg to a fertile adult in about 3 days, and the adult lifespan is about 15 days. One of the most difficult challenges of studying population dynamics in an ecosystem is the time necessary to observe generational cycles, so this aspect of *C. elegans* biology makes it an ideal choice. A typical population dynamic experiment that lasts 100 days includes many generational cycles of *C. elegans*. In our experience, this system makes it possible to sustain and periodically measure *C. elegans* populations for months. We anticipate that the population could be sustained indefinitely with regular maintenance. We refer to this as a **laboratory population**, and it has the essential features of a simple ecosystem described above.

Environment of the laboratory population: The environment for the laboratory population can be considered in two time phases: initialization and maintenance. To **initialize** the environment, we add (1) 5 mL of a simple salt solution with cholesterol called S-Medium⁹ to a 50 mL plastic culture bottle, and (2) 10 mg of *E. coli* bacteria that were grown overnight in nutrient

medium and then concentrated by centrifugation. To **maintain** the environment, we periodically remove 10% of the volume (0.5 mL) and replace it with an equal amount of S-Medium medium (0.5 mL) containing concentrated *E. coli*. We refer to the volume removal as culling, because it removes *C. elegans* and bacteria as well as the liquid medium. To **measure** the environment, we use a spectrophotometer to determine the optical density (OD600), which is proportional to the number of *E. coli*. We convert the OD600 value to a concentration of *E. coli* bacteria (mg/mL) using a standard curve (Figure 1A, Supplementary Figure 1).

While the environment is initially S-Medium, we think that over time the presence of live *E. coli* and live *C. elegans* conditions the medium with complex chemicals, such as waste products and pheromones, as well as debris from dead worms. We think these chemicals gradually accumulate and eventually reach a steady state as a result of periodic culling and feeding. We have not experimentally determined the composition of the medium over time, so we do not know the number and nature of these chemicals or the time necessary for their concentrations to come to equilibrium.

Animals in the laboratory population: To **initialize** animals, we add about 250 *C. elegans* larvae to the culture medium. No other *C. elegans* are added during the experiment, so all additional *C. elegans* in the laboratory population are progeny of these hermaphrodites or their descendants. To **measure** animals, we remove a sample of the laboratory population by culling. Culling can be considered a form of extrinsic mortality, which in natural ecosystems results from predation, disease, accidents, or other causes. For example, in the Serengeti a migrating wildebeest might accidentally drown crossing the Mara River, or it might be predated by crocodiles during the crossing. Culling can also be considered as a form of outmigration, which is also typical of natural ecosystems. An aliquot of the sample derived by culling is analyzed using a COPAS biosort designed for automated counting of *C. elegans*, or by visual inspection using a dissecting microscope (Figure 1A, Supplementary Figure 1). The COPAS biosort instrument flows worms

in liquid past a laser detection system. As worms pass the laser, the animal's body blocks light transmission, and a detector measures the duration of the interruption, called the time of flight. Time of flight is proportional to the length of the worm, an indication of the developmental stage of the animal. This instrument allows high throughput analysis of samples, making it possible to monitor many different populations in parallel. However, the information from this system is limited. Time of flight does not accurately determine the stage of the animals, so while a positive signal indicates the presence of a worm, we do not know the precise developmental stage of that animal. In addition, the COPAS biosort does not reliably give a positive time of flight for eggs because of their small size. Thus, the COPAS biosort measures the number of larvae and adults in the culture. Visual inspection with a dissecting microscope provides detailed information about the number and stage of the animals, including the number of dauer larvae, since stages can be scored by a trained observer. However, visual inspection cannot be performed with high throughput. We used visual inspection to validate that the COPAS biosort provides reliable measurements of the number of larval and adult worms.

Data analysis and summary statistics in the laboratory population: The laboratory population displays two phases of population dynamics, which we named the **initialization** phase and the **maintenance** phase. (1) During the **initialization** phase, the number of worms in the population increases to a uniquely high peak. The initialization phase begins when the experiment begins, and we define the end of the initialization phase as the time when the population first declines to the average number of worms for the experiment. The initialization phase is characterized by three summary statistics: time to first peak, number of worms at first peak, and duration of initialization phase (Figure 1B). The initialization phase displays these unique characteristics because bacterial food accumulates during the first several days of the experiment due to the small number of worms used to begin the culture; as the number of worms increases, the worms eventually ingest the accumulated food as they approach the high first peak. When

the accumulated food is consumed, then the number of worms in the population begins to decline.

(2) During the **maintenance** phase, the number of worms in the population stabilizes and oscillates around the average number of worms. The maintenance phase is characterized by three summary statistics: number of worms at highest peak (maximum), number of worms at lowest valley (minimum), and duration of maintenance phase (Figure 1B). The initialization phase and maintenance phase together represent the entire laboratory population experiment, which is typically 100 days. The entire experiment is characterized by one summary statistic: the average number of worms (Figure 1B). It is also possible to compute the average number of worms in the initialization phase and the maintenance phase separately.

The number of worms at highest peak and number of worms at lowest valley are informative summary statistics because they describe the resilience of a population. If a population displays a small number of worms at the lowest valley, then the population is at higher risk of extinction, which is defined as 0 worms at the lowest valley. The ratio of the number of worms at highest peak and number of worms at lowest valley is an important measure of dynamic volatility that may also have implications for the risk of extinction.

Supplementary section 2:

ODD description of the wormPOP computational simulation

The description of the individual-based model wormPOP follows the Overview, Design concepts, and Details (ODD) protocol^{10,11}. More details are described in the Methods and Supplementary Section 3 and 4 3 in the Supplementary Material.

Purpose

The purpose of the individual-based model wormPOP is to simulate the population dynamics of the nematode worm *C. elegans* cultured in a simple laboratory system. The laboratory population and wormPOP simulation include only two species – individual worms are the

agents, and *E. coli* bacteria are the food source. wormPOP is designed to facilitate the investigation of how environmental factors - bacterial food and culling - and the life history traits of individuals impact population dynamics. The analysis of the laboratory population is limited to population level measurements, since the behavior of individuals cannot be tracked. wormPOP is designed to provide a more detailed examination of individual worms based on explicit laboratory measurements of these behaviors, and aggregates the behaviors to predict population dynamics and demography. Specifically, wormPOP (1) tracks the life history of every individual worm (2) outputs data for the average behavior of individuals, and (3) combines individual behaviors to generate the emergent properties of population dynamics.

wormPOP employs strict conservation of mass, since worms can only grow and reproduce by consuming the *E. coli* food source. The model was designed to have the capacity to investigate how fluctuations in food supply influence population dynamics. wormPOP uses culling to model extrinsic mortality. A purpose of the model is to investigate how the extent and stage-specificity of culling influence population dynamics. wormPOP allows the life history traits of the simulated worms to be modified to create mutant worms. This design feature allows the model to be used to investigate how specific life history traits of an individual affects the emergent property of population dynamics. Thousands of *C. elegans* mutants exist in extensive collections of laboratory strains, and the model is designed to make it possible to simulate the population dynamics of mutant worms in the laboratory population. wormPOP is based on conceptualizing the life cycle of *C. elegans* as a flux system, and it was designed to output the life cycle data in an intuitive graphical form. The model was designed to have the capacity to investigate how environmental factors and life history traits of individuals influence the life cycle flux system. The overall purpose of wormPOP is to be a tool that connects two levels of biological organization – the life history traits of individual animals that are generated during development and the emergent property of population dynamics in an ecosystem.

Entities, state variables, and scales

wormPOP contains two entities: (1) The agents are individual *C. elegans* hermaphrodites (worms), the first species in the simple ecosystem, and (2) the environment includes one entity: *E. coli* bacteria that is the second species in the simple ecosystem.

The state variables or attributes that characterize each individual worm are as follows: (1) identity number – each worm is monitored as a unique individual. (2) Life cycle stage. The lifecycle contains five developmental stages of worms: egg, larva, dauer, adult, and parlad (parent/larva/dauer). Each live worm is in only one of these five stages at a time, and worms progress through stages as they mature. (3) Previous life cycle stages the worm has occupied. This can affect behavior; for example, a worm can only enter the dauer stage once. (4) Age (hours) spent in each developmental stage, which can be used to determine age (hours) since it entered the simulation, (5) Mass (ng) of worm soma at each time step, (6) Mass (ng) of unlaid eggs in adult stage animals at each time step, and (7) Food consumption history for the most recent two time steps. This information affects the probability of a larva transitioning to dauer or the probability of an adult transitioning to parlad.

The environment volume is 5 ml of liquid, which is based on the laboratory population. The environment contains the bacteria, the second species in the ecosystem and food source for worms. The volume of the environment is only relevant in determining the bacteria concentration. The environment is characterized by the state variable of bacteria concentration (ng/ml).

wormPOP operates in discrete time steps that represent 3 hours. This time resolution is well suited for this simulation based on the duration of the life cycle stages and egg laying rates of *C. elegans*. By contrast to the 24-hour time resolution of the laboratory population, 3 hour time

steps allows more detailed data collection. wormPOP was typically run for 100 days (800 time steps).

Process overview and scheduling

In each time-step of the simulation, the environment and the worms proceed through the following processes.

- (1) The user-programmable feeding and culling schedule is consulted. If applicable, feeding/culling is performed at the beginning of the time step.
 - a. If the culling schedule calls for it, then worms are culled (removed from the simulation by extrinsic mortality) and/or bacteria are culled (removed from the simulation). Worms are randomly selected for culling based on their stage and according to a specified percentage of the group. This is implemented in code as a separate random probability that each worm at whatever stage will be removed from the system. Individual life histories of worms are updated, specifying cull as the cause of death. The state variable of bacteria concentration in the environment is updated.
 - b. If the feeding schedule calls for it, then a specified amount of bacteria (ng) is added, and the state variable of bacteria concentration in the environment (ng/ml) is updated.
- (2) The “appetite” of every worm is computed. This is the amount of food it would eat if food were plentiful. The sum of appetites is used later to assure approximately uniform access to food, independent of computational ordering of the worms’ eating behavior.
- (3) The worms’ behaviors are considered one-by-one, in random order, depending on the life stage and history which each worm retains.

a. Eggs stage progress: eggs can remain eggs or transition (hatch) into larva.

Individual life histories of worms are updated, specifying developmental stage.

b. Larva:

- i. Larva stage progress to dauer or starve: If larva don't get enough food, they transition to dauer or die of starvation. Individual life histories of worms are updated, specifying developmental stage or starvation as cause of death.
- ii. Larva ingest bacteria: Worms in the larva stage ingest bacteria based on age, mass, the bacteria concentration in the environment and the appetite of other worms. Individual life histories of worms are updated, specifying bacteria ingested at time step.
- iii. Larva use ingested mass for maintenance and growth. Individual life histories of worms are updated, specifying mass used for maintenance, growth, and growth efficiency loss.
- iv. Larva stage progress to adult or starvation: larva can transition into adults or die of starvation. Individual life histories of worms are updated, specifying developmental stage.

c. Dauer:

- i. Dauers do not eat or grow or lay eggs. They only test the environment for available food and if it is greater than the (user-programmable) threshold, the dauer returns to the same larval stage and picks up just where it left off before it was a larva, with the same history and the same mass. (Note that the probability of this dauer transition to larva is dependent on the food available at the moment that this worm's turn comes up in the random ordering, so to this extent it is stochastic.)

- ii. Dauers stage progress to larva or starve: dauers can transition into larva based on the bacteria concentration. If dauers don't sense food for too long, they die of starvation. Individual life histories of worms are updated, specifying developmental stage or starvation as cause of death.
- d. Adult:
 - i. Adults ingest bacteria: Worms in the adult stage ingest bacteria based on age, mass, the bacteria concentration in the environment and the appetite of other worms. Individual life histories of worms are updated, specifying bacteria ingested at time step.
 - ii. A fraction of the mass is consumed in metabolism. The consumed food is apportioned between growth and egg mass.
 - iii. Adults use ingested mass for maintenance, growth and egg-laying: Individual life histories of worms are updated, specifying mass used for maintenance, growth, growth efficiency loss, eggs, and reproductive efficiency loss, and new eggs are added to the simulation as new individuals.
 - iv. Adults die of starvation and transition to parlard: If adults don't get enough food, they die of starvation. Individual life histories of worms are updated, specifying starvation as the cause of death and transition to parlard.
 - v. Adults die of old age: If adults reach a specified age, they die from intrinsic causes called old age. Individual life histories of worms are updated, specifying old age as the cause of death.
- e. Parlards stage progress: parlards can remain parlards or transition (burst) into dauers. Individual life histories of worms are updated, specifying developmental stage or death by starvation when the parlard bursts. When parlards burst, new dauers are added to the simulation as new individuals.

Various bookkeeping functions are performed, including removal of dead worms from the roster.

Design concepts

Basic principles

To exploit the power of individual-based models, we designed a simple laboratory population to be amenable for simulation. Several features make the population well suited for modeling: (1) The ecosystem includes only two species – each nematode is an individual, and the *E. coli* bacteria considered as a whole is one entity. (2) We can measure the population dynamics of worms and bacteria in the laboratory population, resulting in quantitative benchmarks for the behavior of the simulation. (3) We can measure the properties of individuals in conditions very similar to the laboratory population, which allows realistic simulations of individual behavior. The individual-based model complements the laboratory population by simulating the behavior of each individual worm in the population and allowing detailed analyses of the population with 3-hour resolution. Furthermore, we conceptualized the *C. elegans* life cycle as a flux system that links individuals to population phenomenon, and generated an intuitive graphical output that shows the flux of individuals through the life cycle. We implemented mass conservation, which is critical for long term studies of population dynamics. By using laboratory measurements of growth and reproduction at different environmental bacterial concentrations, the model incorporates the plasticity of individual worm responses to variable food environments. Details are in Supplementaru Section 3.

Emergence

For bacteria, the input frequency and amount are determined by a user programmable input, and culling frequency and percent are determined by a user programmable input. The emergent properties of bacteria include (1) the concentration at each time step (size of bacterial node), (2)

amount ingested by larvae at each time step: $bt(b>l)$, (3) the amount ingested by adults at each time step: $bt(b>a)$, and (4) the amount culled at a relevant time step: $bt(b>c)$.

For individual worms, many traits such as growth and reproduction depend on the food environment. Thus, the detailed life history of each individual worm is an emergent property based on the fluctuating food environment during its lifetime and stochastic events such as entry into dauer or culling. Similarly, the average behavior of worms in the simulation, such as the average egg laying curve of all adults, is an emergent property, based on analyzing many different individuals, each of which has a life history with emergent properties.

All of the population dynamic values are emergent properties, including the size of each worm node at each time step and the worm transition (wt) rates at each time step, which can be calculated as worm number or worm mass.

Adaptation

Larvae and adult worms display bacteria ingestion, growth and egg laying plasticity that depends on the bacteria concentration. Larvae display transition into adult, dauer or starvation based on bacteria concentration. Adults display transition to parlad based on bacteria concentration. Dauer display transition into larvae or starvation based on bacteria concentration.

Sensing

All worm individuals are assumed to sense the bacterial concentration. Individuals are simply assumed to know this state variable.

Interaction

Individual worms interact directly with bacteria, since worms ingest bacteria as food. Worms do not interact directly with other worms; however, worms interact indirectly with other worms through the shared bacterial food source. For example, if one worm ingests bacteria, it is no longer available as a food resource for other worms.

Stochasticity

Stochasticity in the model is limited to:

- (1) Culling, in which each individual is subjected individually to a constant probability of culling at programmed intervals.
- (2) Life stage transitions: larva to and from dauer and adults die of old age are controlled by probability functions.
- (3) At each time step, the order of analyzing the worms is randomly determined using stochastic probability.

Observation

In each simulation, detailed information regarding the bacteria in the environment, the individual worms, and the population of worms are collected and saved. (A) For the environment, the simulation collects and saves the bacteria concentration at the beginning of each time step and the bacteria transition (bt) rates. (B) For the individual worms, the simulation collects and saves age, developmental stage, mass, and laid and unlaid egg mass at each time step, as well as cause of death. The fate of all ingested mass of each individual is collected and saved, including mass that was used by larvae and adults for growth, maintenance and efficiency loss. (C) For the population of individual worms, the simulation collects and saves the size of each node and the worm transition (wt) rates at each time step, measured in both number and mass.

Initialization

The initial state of the model world is specified by the initial amount of bacteria and the initial number and stage of worms. These are user programmable inputs that can be varied. Simulations were initialized with 5 or 10 mg bacteria. Simulations were initialized with 250 or 1000 eggs, larva, or dauer. The state variables of eggs are a mass of 65 ng, they have been 1 to 5 time steps in the egg stage and hatch after 5 time steps. The state variables of larvae are 228 ng and they are 0 – 5 time steps in the larva stage. The state variables of dauer are a mass

of 228 ng and they 5-15 time steps in the dauer stage. The initial variables were chosen to match the laboratory population.

Input data

Input data for the wormPOP model is periodic addition of bacteria and culling, and the frequency and amount is user programmable. Bacteria were added and culling was performed every 24 or 48 hours to mimic the laboratory population.

Submodels

All submodels and parameters (traits) are described in detail in the Methods and Supplementary Section 3 and in Supplementary Table 18, 21, 22. Submodels of the environment are “culling” and “adding bacteria”. Submodels of the individual worms are specific to worm stages and describe worm behavior or worm transitions: (1) Eggs behave according to the submodels “culling” and “hatching”; (2) Larva behave according the submodels “culling”, “ingestion”, “starvation”, “cost of living”, “growth”, “larva transition into dauer”, and “larva transition into adults”; (3) Dauers behave according the submodels “culling”, “dauer transition into larva”, and “starvation”; (4) Adults behave according to the submodels “culling”, “ingestion”, “cost of living”, “growth”, “egg-laying”, “adult transition into parlad”, and “die of old age”; (5) Parlays behave according to the submodels “culling” and “parlad transition into dauers”.

Supplementary Section 3: Comparison of the laboratory population and the computational simulation

Development of an individual-based model: To complement the laboratory population, we developed a computational simulation. Our goal was to develop a realistic simulation of the laboratory population. This task was facilitated by our decision to design the laboratory population

to be well suited for simulation by an individual-based model. Like all models of biological systems, this simulation is a simplification of reality. However, in designing the simulation, we attempted to retain the essential elements of reality while simplifying when precision did not appear to be critical to the function of the system or when simplification was a practical approach to address a complex reality. The simulation has several advantages compared to the laboratory population, and together they form a powerful combination of experimental approaches to understand a complex system. The simulation offers two main advantages: (1) It provides detailed information about the life history of individual animals, which cannot be measured in the laboratory population. (2) The simulation makes it possible to model a wide range of different environments and mutant worms with different traits. The laboratory population offers a limited ability to create different environments and a limited ability to investigate worm traits by analyzing mutant strains.

We chose to use an individual-based (also called agent-based) model to simulate the laboratory ecosystem¹². Individual-based models consist of an environment and agents. In our simulation the agents are worms. The behavior of agents is determined by a series of rules, which can be considered as if/then statements or decision trees. For worms, these rules specify behaviors such as feeding and egg laying, transitions between developmental stages, transition to death, etc (Extended Data Figure 1). The computational simulation traces the life history of each individual worm by accounting for (1) biomass ingested as bacterial food, and (2) biomass spent as energy or converted into growth, eggs, or dauers. To calibrate parameters in the computational simulation, we measured single worm characteristics in the laboratory (Figure 2, Supplementary Figure 2-7, Supplementary Table 3-6). Parameters of the model were fitted to these measurements where available. Some parameters could not be measured in the laboratory; in these cases the parameter values were merely reasonable guesses (Supplementary Table 18, 22).

The second aspect of an individual-based model is the environment. The simulated physical environment is 5 mL of liquid medium. The medium contains bacteria at a concentration that can be calculated. The concentration of bacteria influences the behavior of the worms. Worms in the simulation do not interact directly, so we do not consider worms to be a part of the environment. However, worms do interact through the common bacterial food source, such that if worm #1 ingests bacterial food, that bacteria is not available for ingestion by worm #2. Time is quantized in 3-hour intervals, so that bacteria consumption, growth, and all life stage transitions are updated every 3-hour time period. We chose three hours because it is a relatively short time compared to the three day (72 hour) generation time, so it provides good granularity for the trajectory of each individual. Shorter time periods provide additional granularity but are more computationally demanding.

Environment of the computational simulation: The environment for the computational simulation can be considered in two phases: initialization and maintenance. To **initialize** the environment, the computational simulation adds a specified mass (mg) of *E. coli* bacteria to the virtual 5 mL volume (Supplementary Table 19). To **maintain** the environment, the computational simulation periodically remove a specified percent of the *E. coli* bacteria (culling), and adds a specified mass (mg) of *E. coli* bacteria (feeding) (Supplementary Table 20). To **measure** the environment, the computational simulation calculates the mass of bacteria in the bacterial node at the beginning of each time step.

The simulation permits a variety of programmed schedules for feeding and culling. Feeding is specified by two variables: (1) The mass of bacteria added. (2) The frequency of addition. Culling is specified by three variables: (1) The fraction of animals/bacteria culled. (2) The stage of animals culled. (3) The frequency of culling. It is assumed that the population is well mixed; therefore, if all-stage culling is chosen, then an equal amount of each stage will be culled. For example, if 10% all-stage culling is the user-programmable parameter for a simulation, then

the model assumes that 10% of all eggs, 10% of all larvae, 10% of all dauers, 10% of all adults, and 10% of all parlads are removed, along with 10% of the uneaten bacterial food remaining from previous feedings. All-stage culling corresponds to the culling procedure performed in the laboratory population. The simulation also has the option of stage-specific culling, which cannot be achieved in the laboratory population. This option is useful for modeling single generations without contamination from offspring and for creating conditions in which old age as a cause of adult death can become significant.

In the computational simulation, bacteria exist in the bacterial node. Bacterial transitions (bt) can cause bacteria to enter or leave the bacterial node. There is only one way for bacteria to enter the bacterial node: **(1) A user-programmable input (i) for bacteria (b) named $bt(i>b)$.** There are three ways for bacteria to leave the bacterial node: **(1) Bacteria (b) can be ingested by a larva (l) in a transition named $bt(b>l)$.** The amount of bacteria that a larva ingests is determined as described below. **(2) Bacteria (b) can be ingested by an adult (a) in a transition named $bt(b>a)$.** The amount of bacteria that an adult ingests is determined as described below. **(3) Bacteria (b) can transition to death by culling (c) in a transition named $bt(b>c)$.** The percent and frequency of bacteria culled is a user-programmable environmental parameter.

The major features of the laboratory population environment are modeled realistically in the simulation. The environments of the computational simulation and laboratory population have the identical volume, and the bacterial feeding and culling frequencies and amounts can also be programmed to be identical to the laboratory population. One difference between reality and simulation is that we think live *E. coli* and live *C. elegans* condition the laboratory population medium with complex chemicals, such as waste products and pheromones, as well as debris from dead worms. Because we do not know the composition or consequence of these chemicals, we did not attempt to simulate this feature of the environment. Furthermore, the laboratory

population experiences small fluctuations in environmental conditions such as temperature and humidity, whereas the simulation is assumed to be constant.

Animals (agents) in the computational simulation: Worms were defined as being in one of five life stages: egg, larva, dauer, adult, or parlad (parent/larva/dauer). *C. elegans* has four larval stages during reproductive growth, L1, L2, L3, and L4, and one larval diapause stage called dauer. Worms transition between larval stages by molting. We chose to simplify the larval stages rather than specific every larval molt.

Egg: *C. elegans* hermaphrodites produce oocytes in the gonad that are fertilized by sperm in the spermatheca; the fertilized egg begins development as it passes through the uterus and is typically laid in the environment at the 32-128 cell stage. Eggs are provisioned with adequate nutrients to support development and do not ingest nutrients. The eggshell protects the developing embryo from the environment. The purpose of the life stage is to accomplish development from the fertilized single cell to the L1 larva. When development is complete, the L1 larva emerges and the egg shell is shed.

In the computational simulation, eggs are derived from one source: **(1) An adult (a) can lay an egg (e) in a transition named $wt(a>e)$** . All eggs have a mass of 65 ng; this value is based on laboratory measurements of L1 size, which were converted to mass (65.6 ng +/-11, n=4 N=166). Eggs do not eat bacterial food and do not use mass for maintenance; thus, the mass of an egg remains constant over time. Eggs can transition to two fates: **(1) An egg (e) can transition to a larva (l) in a transition named $wt(e>l)$** . An egg hatches after 15 hours (5 time ss), at which time it transitions to a larva with a mass of 65ng. The time to hatching was based on laboratory measurements (15 hours +/-1, n=4). **(2) An egg (e) can transition to death by culling (c) in a transition named $wt(e>c)$** . The percent and frequency of eggs culled is a user-programmable parameter.

The simulated eggs behave realistically, since the mass of an egg and the duration in the egg stage are the two main traits, and both were measured in the laboratory. The assumption that no mass is lost when an egg transitions to a larva is a simplification, since there is likely a small loss of mass when the egg shell is shed, and the efficiency of conversion between yolk and L1 larva is likely less than 100%. The assumption that all eggs have the identical mass and duration as eggs is a simplification, since there is some variability between individuals.

Larva: The larva is a feeding stage whose main biological imperatives are to ingest bacteria, grow, and transition to a sexually mature adult, all the while surviving periods of nutrient deprivation or other harsh conditions. When an L1 larva emerges from the egg, it is highly starvation resistant. As it begins to feed and grow, it becomes more vulnerable to starvation. With adequate nutrition, it molts to form an L2 larva. A L2 larva grows and molts into a L3 larva or a dauer larva, depending on environmental factors including the level of food, level of dauer pheromone, and temperature. The dauer larva is discussed below. With adequate nutrition, a L3 larva grows and molts into a L4 larva, the final larval stage. The L4 larva is characterized by growth and development of the reproductive system. With adequate nutrition, a L4 larva grows and molts into a sexually mature adult. The larval growth rate, and the size and mass of the larva at the L4 to adult transition, are highly dependent on the concentration of bacterial food in the environment.

In the computational simulation, larvae are derived from two sources: **(1) When it hatches, an egg (e) transitions to a larva (l) in a transition named $wt(e>l)$.** The mass of the larva is 65 ng, and the age is zero time steps. **(2) A dauer (d) transitions to a larva (l) in response to high levels of bacterial food in a transition named $wt(d>l)$.** The mass and age of the larva are equal to the mass and age of the larva that formerly transitioned into dauer, which can be different for each animal.

A larva (l) eats bacterial (b) food in a transition named $bt(b>l)$. The amount of bacterial food that a larva eats depends on three variables – the mass of the larva, the concentration of

bacterial food in the culture medium, and the number of worms in the population. Food that a larva ingests is used in two ways: growth and maintenance. The growth rate of larvae in different concentrations of food was measured in the laboratory (Figure 2E-H, Supplementary Figure 2B, 3). These measurements were used to determine how much simulated worms eat and grow, as described below. The amount of food used for maintenance is a reasonable guess.

Larvae can transition to four fates: **(1) A larva (l) can transition to an adult (a) in a transition named $wt(l>a)$** . When bacterial food is abundant, a larva transitions to an adult after 20 time steps =2.5 days if it has achieved a minimum mass of 800 ng. If bacterial food is not abundant, then a larva grows more slowly and it can transition to an adult when it attains a minimum mass of 800 ng from time step 21-28 (3.5 days). The time of larval transition to adult and mass of the larva at the transition were based on laboratory measurements of growth and maturation (Figure 2E-H, Supplementary Figure 2B, 4, Supplementary Table 4). **(2) A larva (l) can transition to a dauer (d) in a transition named $wt(l>d)$** . A larva has a specified probability of turning into a dauer if it experiences two successive time periods in which the bacterial food concentration is less than 0.05 mg/mL and the mass of the larva is between 0.6 and 2.0 times the standard dauer mass (equivalent to 136 – 457 ng). Standard dauer mass is fixed from worm parameters as the geometric mean between larva mass on hatching (65 ng) and minimum adult mass (800 ng). The geometric mean of 65 and 800 is 228 ng. The duration of low bacterial food that leads to a dauer transition and the mass range for larva that can transition to dauer are reasonable guesses. The actual probability of a larva transitioning to a dauer per unit time is computed by a formula shown in Supplementary Table 18. A larva cannot transition to become a dauer a second time. **(3) A larva (l) can transition to death by starvation (s) in a transition named $wt(l>s)$** . A larva starves if it experiences two successive time periods in which bacterial food concentration is less than the dauer food threshold defined above and the mass of the larva is outside the range for dauer transitions (65-136 ng or 457-799 ng). A larva also transitions to starvation death if their age exceeds 28 time steps and they have not attained the minimum adult

mass of 800 ng. The duration of low bacterial food that leads to a starvation transition and the mass range for larva that can transition to starvation are reasonable guesses. **(4) A larva (l) can transition to death by culling (c) in a transition named $wt(l>c)$.** The percent and frequency of larval culling is a user-programmable parameter.

The simulated larvae are fairly realistic. The growth rate of larvae in different concentrations of food and the transition to sexually mature adults were measured in the laboratory and are well modeled in the simulation. The environmental conditions that trigger starvation and transition to dauer are reasonable guesses that may be too stringent or lenient. The model does not include dauer pheromone, which is a simplification since it is established that pheromone influences the probability of larva transition to dauer ¹³. The assumption that all larva that are too small or too large to transition to dauer have the same thresholds for starvation is a simplification, since newly hatched L1 larvae are known to be highly starvation resistant, and each larval stage may have a different ability to resist starvation. The assumption that larvae starve if they fail to achieve the minimum adult mass after some period of time is reasonable, but this time could not be measured and is a guess. The assumption that a certain amount of biomass is consumed for metabolic function is undoubtedly true, but the precise amount could not be measured and the simulated amount is a guess. Likewise, the assumption that ingested bacterial biomass is converted to worm mass during growth at less than 100% efficiency is undoubtedly true, but the precise efficiency could not be measured and the simulated efficiency is a guess. As described in Supplementary Section 4, we guessed the value of these two parameters by calibrating the simulation with a training set of laboratory ecosystem data.

Dauer: The dauer is an alternative L3 larval stage considered a diapause state. L2 larvae molt to form dauer larvae under harsh environmental conditions, such as low levels of food, high temperature, and high levels of dauer pheromone that signal a high density of worms ¹³. The dauer larvae do not feed, and they have a cuticle that is resistant to chemical insults. The dauer

larvae are metabolically active and monitor their environment, such that they will transition to the reproductive L4 larval form in response to high levels of food in the environment. They also engage in behaviors that promote dispersal. Thus, dauers must consume energy to sustain their metabolic activity, and although they are long lived, they cannot survive indefinitely. The biological imperative of the dauer is to survive periods of stress and deprivation and disperse, so that they can emerge when conditions improve and initiate a new population.

In the computational simulation, dauers are derived from two sources: **(1) A larva (l) transitions to a dauer (d) in response to low levels of bacterial food in a transition named $wt(l>d)$** . The mass and age of the dauer are equal to the mass and age of the larva that made the transition. **(2) A parlad (p) transitions to a dauer (d) in a transition named $wt(p>d)$** . The mass and age of a dauer derived from a parlad is equal to 228 ng and 5 time steps. Thus, dauer is a response to low levels of bacterial food. A dauer does not eat bacterial food and does not use mass for maintenance; thus, the mass of a dauer remains constant over time.

A dauer can transition to three fates: **(1) A dauer (d) can transition to a larva (l) in a transition named $wt(d>l)$** . A dauer will transition to a larva and resume growth if there is a sufficient concentration of bacterial food. The probability per time period for a dauer transitioning to a larva is determined by a formula shown in Supplementary Table 18 independent of how long it has been a dauer. This is based on laboratory measurements of dauer to larva transitions in different concentrations of bacterial food (Figure 2I-L, Supplementary Figure 2C, 5, 6, Supplementary Table 5). A dauer “remembers” the mass and age that it had when it transitioned from a larva or a parlad when it resumes life as a larva. The time spent as a dauer does not count toward the time limit to reach maturity. **(2) A dauer (d) can transition to death by starvation (s) in a transition named $wt(d>s)$** . Over time, dauers lose the ability to transition into a larva . The model accounts for this gradual loss of viability by including an increasing age-dependent probability that a dauer will die of starvation. Thus, a low percentage of dauer selected randomly will die of starvation in each time-step (Supplementary Table 17). **(3) A dauer (d) can transition**

to death by culling (c) in a transition named $wt(d>c)$. The percent and frequency of dauer culling is a user-programmable parameter.

The simulated dauer are fairly realistic. The bacterial concentrations that trigger dauer to larva transitions were measured in the laboratory and are accurately modeled in the simulation. The assumption that a dauer does not consume biomass for metabolic function is a simplification, but given the longevity of a dauer the rate of consumption must be small. The model does not include dauer pheromone, which is a simplification since it is established that pheromone influences the probability of a larva transitioning to a dauer ¹³.

Adult: The sexually mature adult hermaphrodite is the reproductive form. The hermaphrodite gonad first produces about 350 self sperm, which are stored in the spermatheca. Next the gonad begins to produce oocytes, and self sperm are used to fertilize oocytes. Adults with abundant bacterial food produce large numbers of progeny in the first several days, and then progeny production declines due to reproductive aging and sperm depletion. Adults must ingest bacteria to obtain the biomass to generate eggs. Thus, the biological imperative of the adult is to eat and produce eggs. If the sensory system of the adult determines that bacterial food levels are very low, then the adult will execute a behavioral program that causes it to cease egg laying ^{14,15}. After about 15 hours, the fertilized eggs will hatch inside the hermaphrodite, an event called matricidal hatching that leads to adult death. Adults display age-related degeneration, which leads to a mean lifespan of about 15 days.

In the computational simulation, adults are derived from one source: **(1) A larva (l) can transition to an adult (a), in a transition named $wt(l>a)$.** As described above, a larva transitions to an adult if it grows to a mass of more than 800 ng between time steps 20-28. The mass of the adult at the transition is equal to the mass of the larva that made the transition. The adult age at the time of transition is 0 time steps.

An adult eats bacterial food in a transition named $bt(b>a)$. The amount of bacterial food that an adult eats depends on four variables – the mass of the adult, the age of the adult,

the concentration of bacterial food in the culture medium, and the number of worms in the population. Food that an adult ingests is used in three ways: growth, maintenance, and generating eggs. The growth rate of adults in different concentrations of food was measured in the laboratory (Figure 2E-H, Supplementary Figure 2B, 4, Supplementary Table 4). These measurements were used to determine how much simulated worms eat and grow, as described below. The amount of food used for maintenance is a reasonable guess.

The rate of egg laying in different concentrations of food was measured in the laboratory (Figure 2A-D, Supplementary Figure 2A, 3, Supplementary Table 3). These measurements were used to determine how much simulated adult worms eat and lay eggs. A nine-parameter function controls the number of eggs laid as a function of adult age and bacterial food concentration. The function was fitted to data points measured daily in the laboratory at six different bacterial concentrations (Figure 2A-D, Supplementary Figure 2A, 4). Explicitly, the number of eggs laid in a 3-hour period is given by $M x^n \exp(-x)$, where x is adult age scaled by a suitable parameter. The three parameters M , n , and scale are all modeled as power law functions of adult age, of the form

$$M = A_M \text{age}^{B_M} + C_M$$

$$n = A_n \text{age}^{B_n} + C_n$$

$$\text{scale} = A_{\text{scale}} \text{age}^{B_{\text{scale}}} + C_{\text{scale}}$$

The nine parameters A , B and C are for best conformity with laboratory data on fertility. The values we computed via this process are shown in Supplementary Table 18. Supplementary Figure 18A shows one example of the close correspondence between the laboratory data for egg laying and this nine-parameter function for the bacterial food concentration 0.5 mg/mL.

Supplementary Table 16. Values of nine-parameter function that controls progeny production.

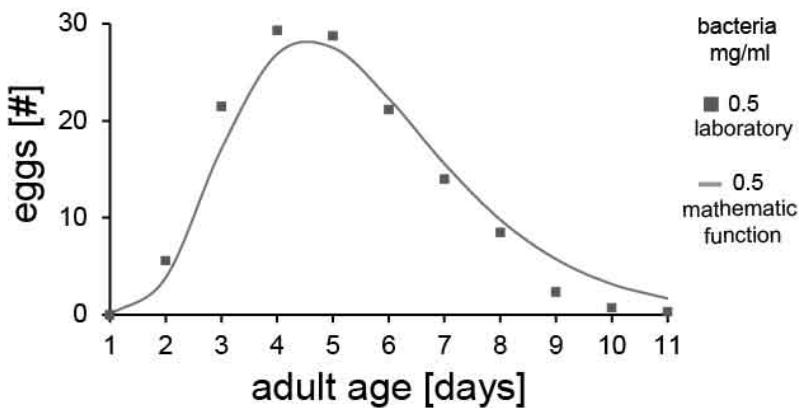
	Scale¹	n²	M³
A	0.233	-1.867	-17.33
B	-0.762	-0.299	-0.166
C	0.581	5.908	30.08

$$^1 scale = A_{scale} age^{B_{scale}} + C_{scale}$$

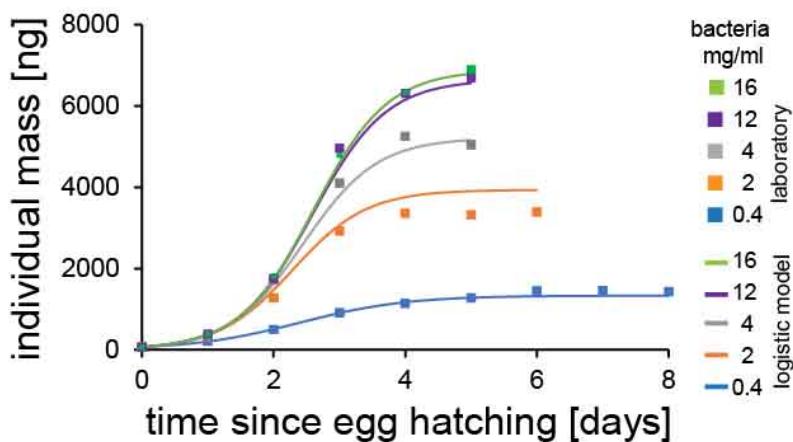
$$^2 n = A_n age^{B_n} + C_n$$

$$^3 M = A_M age^{B_M} + C_M$$

A



B



Supplementary Figure 18. Comparison of laboratory data and logistic models of daily progeny production and growth. Wild-type, self-fertile hermaphrodites were cultured in S-Medium with the indicated concentrations of *E. coli* (bacteria). (A) Average daily progeny production of individual adults measured in the laboratory is displayed as grey boxes. The same data are displayed in Figure 2A-D, Supplementary Figure 2A, 3. The gray line shows one example of the nine-parameter function that we calculated to describe these data for the bacterial food concentration 0.5 mg/mL. There is a close correspondence between the laboratory data for egg laying and the mathematical formula. (B) The average daily mass of individual animals measured in the laboratory is displayed as color boxes. The same data are displayed in Figure 2E-H, Supplementary Figure 2B, 4. The color lines show examples of the logistic model for five different bacterial food concentrations. The lines correspond well with the laboratory data with the same concentration of *E. coli*.

An adult can transition to three fates: **(1) A adult (a) can transition to a parlad (p) in a transition named $wt(a>p)$** . If total food in the environment falls below a threshold of 500 ng/mL for two successive time periods, then an adult transitions to a parlad. In response to food deprivation, self fertile adults stop laying eggs and undergo matricidal hatching^{14,16}. Thus, the transition to parlad is a form of starvation death. Eggs that hatch into larva inside the adult begin to feed on the adult biomass, ultimately generating dauer larva^{14,16}. The parlad has the same mass as the adult. The level and duration of low bacterial food that leads to a parlad transition is a reasonable guess. **(2) An adult (a) can transition to death by old age (o) in a transition named $wt(a>o)$** . Death from old age is controlled by a Gompertz curve that was calibrated to laboratory measurements (Figure 2M-P, Supplementary Figure 2D, 7, Supplementary Table 6a). This transition is independent of bacterial food and fertility. Two user-programmable parameters control the timing and the steepness of the Gompertz curve. The probability of dying of old age per unit time is given by $(\exp(\text{age}/\tau)-1) / A$, where age is measured from the transition from larva to adult, in 3-hr periods $\tau = 28.6 A = 168 * (\exp(5) - 1) = 24,765$, where 5 is the number of Gompertz e-foldings in a lifespan. **(3) An adult (a) can transition to death by culling (c) in a transition named $wt(a>c)$** . The percent and frequency of adult culling is a user-programmable parameter.

Simulated adults display realistic growth, egg laying, and adult lifespan, since these are based on laboratory measurements. The threshold and duration of low levels of bacteria that trigger the transition to parlad are reasonable guesses that may be too stringent or lenient. The assumption that a certain amount of biomass is consumed for metabolic function is undoubtedly true, but the precise amount could not be measured and the simulated amount is a guess. Likewise, the assumption that ingested bacterial biomass is converted to worm mass during growth or egg production at less than 100% efficiency is undoubtedly true, but the precise

efficiency could not be measured and the simulated efficiency is a guess. As described in Supplementary Section 4, we guessed the value of these two parameters by calibrating the simulation with a training set of laboratory ecosystem data.

Parlad: If the sensory system of the adult determines that bacterial food levels are very low, then the adult will execute a behavioral program that causes it to cease egg laying^{14,16}. This behavioral response is presumed to be adaptive, since depositing eggs into an environment with low levels of food makes hatching larvae vulnerable to starvation. About 15 hours after the cessation of egg laying, the fertilized eggs in the uterus hatch inside the adult, resulting in matricidal hatching and adult death. Because larvae can ingest the hermaphrodite's soma as a source of nutrition, they can mature inside the adult until they reach the dauer stage^{14,16}. The dead or dying adult hermaphrodite with live progeny inside is a common phenotype called egg-laying defective (Egl), also referred to as a "bag-of-worms". We chose the name parlad (parent/larva/dauer) for this form to emphasize that it is a colony with multiple individuals that are progeny of a single hermaphrodite.

In the computational simulation, parlads are derived from one source: **(1) An adult (a) can transition to a parlad (p) in a transition named $wt(a>p)$.** An adult transitions to a parlad when it ceases egg laying in response to low levels of bacterial food. A parlad does not eat bacterial food and does not use mass for maintenance; thus, the mass of a parlad remains constant over time.

A parlad can transition to two fates: **(1) A parlad (p) can transition to starvation death (s) and generate dauers (d) in transitions named $wt(p>s)$ and $wt(p>d)$, respectively.** The parlad is dead and does not eat. The progeny are alive – the eggs transition to larvae inside the hermaphrodite, the larvae feed on the adult biomass and grow, and finally the larvae transition to dauer^{14,16}. For the simulation, a parlad generates dauers with a mass of 228 ng after 30 hours (10 time periods), at which time the adult transitions to starvation death. The time to dauer generation was guessed and is independent of external conditions. The number of dauers generated is

determined by dividing the adult mass by 228 ng and rounding to the highest whole number. The remaining mass transitions to death by starvation. **(2) A parlad (p) can transition to death by culling (c) in a transition named wt(p>c).** The percent and frequency of parlad culling is a user-programmable parameter.

Growth of larvae and adults: Growth is a function of worm mass and bacterial food concentration in the medium. There is a single, four-parameter function that determines growth, and it is continuous between larval and adult life stages. The function was fitted to daily measurements of worm mass in the laboratory at five different bacterial concentrations (Figure 2E-H, Supplementary Figure 2B, 4, Supplementary Table 4). Explicitly, the form of the function is the logistic equation,

$\frac{dx}{dt} = Kx(1 - bx)$, where K is the exponential growth rate and b is the reciprocal of the terminal mass. Based on laboratory data, we find K is well represented by $K = 1.78 * \tanh(2.13 * food)$, when time is measured in days and bacterial food is measured in mg/mL. b is well represented by $b = 1.30 * 10^{-4} - \frac{2.49 * 10^{-4}}{food}$, where b is measured in reciprocal nanograms and bacterial food is measured in mg/mL. Supplementary Figure 18B shows comparisons of laboratory measurements and this four-parameter function.

Bacterial food ingestion by larvae and adults: The quantity of food a worm eats in a time period is the most complicated function in the simulation. Food ingestion by individual worms is difficult to measure in the laboratory because of the small size of individuals. Therefore, in the simulation ingestion is computed from the growth and fertility curves defined above. We assume that in each time period an individual worm ingests an amount of bacterial food mass that is greater than the amount of mass it grows and/or generates in eggs. There is a user-programmable parameter that determines the efficiency of conversion of biomass. In each time step, a worm is determined to ingest a mass of *E. coli* equal to:

$$\frac{\text{mass it grows} + \text{mass of eggs it lays}}{\text{efficiency of conversion}}$$

For example, if the efficiency of conversion is 50%, and a larva is determined to grow by 5 ng, then the larva will ingest 10 ng of bacterial food. Food ingestion can be limited by either of two things: (1) The worm's intrinsic capacity to ingest food at this stage of life. How much would it eat if food were plentiful? (2) Competition with other worms may be a limit if the number of worms is large. In other words, food concentration may be substantially depleted by other worms during the course of the three-hour time period. The first is represented in a function called "appetite" which computes the worm's needs for growth, egg laying, and metabolism. Growth and egg laying are already functions of food concentration, so they incorporate the worm's limited capacity to filter feed when food concentration is low. Appetite is adjusted by (1/efficiency) to account for metabolic losses in converting food to growth or eggs. The second is a function called "portion", which is computed simply by dividing the worm's appetite by the sum of all appetites of all worms, and multiplying this fraction by the total amount of food in the vial. Specifically, the larva's appetite is computed as a "reduced quantity" based on (x) a fixed fraction of its mass and (y) the amount of food, at present concentrations, that it can filter in 3 hours. The "reduced quantity" is computed as $w = \frac{xy}{(x+y)}$. A further restriction on the amount eaten is the pro-rata portion of food available

computed as the

$$z = [\text{total food}] * [\text{appetite of this worm}] / [\Sigma \text{ appetites of all worms}]$$

The final computation of the amount consumed by this larva is the reduced quantity $\frac{wz}{(w+z)}$. To validate our implementation of bacteria ingestion, we compared the concentration of bacteria in the laboratory ecosystem (Figure 1C) to the simulation (Figure 3C). Both showed qualitatively similar fluctuations with an early peak in the initialization phase and much lower levels during the culture phase.

Data analysis and summary statistics in the computational simulation: The simulation contains two types of data: (1) Detailed life histories of each individual, which are

longitudinal data. (2) Detailed information about the behavior of the population, which are emergent properties determined by the traits of worms and the environment.

For each individual, the simulation records at each time step the stage, mass, bacteria mass ingested, and mass consumed for metabolic maintenance, growth, and egg laying. Thus for each individual it is possible to determine the growth rate as a larva and adult and calculate key summary statistics: mass at sexual maturity, sexual maturity growth span, maximum mass, and maximum mass growth span (Figure 2G, Supplementary Table 2, Supplementary Data 1). For each individual that lays eggs, it is possible to determine the egg-laying curve and calculate key summary statistics: peak progeny number, reproductive span to peak, total progeny number, and total reproductive span (Figure 2C, Supplementary Table 3). It is possible to determine the larval span, dauer span, adult span, age at death and cause of death. Each individual has a flux of mass that can be calculated. Mass flowing into the individual consists of (1) the starting mass of the egg or dauer, and (2) ingested bacterial mass. Mass flowing out of the individual consists of (1) mass consumed for metabolic maintenance, (2) mass converted to growth, (3) mass converted to eggs or dauer, (4) mass consumed in inefficient conversion of bacteria to growth or eggs, and (5) mass remaining at time of death (Supplementary Table 2, Supplementary Data 1). For each individual, the mass flowing in equals the mass flowing out, and it is possible to calculate the percent of mass used for each of the five categories.

For the behavior of the population, it is useful to consider the simulation as a flux system. It is possible to analyze each of the five worm nodes (egg, larva, dauer, adult, and parlad) and calculate the number of individuals in the node at each time and calculate key summary statistics: average worm number, maximum worm number and minimum worm number. Similarly, it is possible to analyze each of the transitions and determine the rate in worms per time. Different transition rates can be compared. For example, adults die of three causes - culling, starvation and old age - and it is possible to calculate the percent of each as a cause of death.

The computational simulation has mass accounting. Mass enters the simulation in two ways: (1) The majority of mass enters through periodic inputs of bacteria. (2) A small amount of mass enters in the form of worms that initialize the population. Mass in the simulation is converted from bacteria to worms through worm feeding. Mass can transition between stages of worms. Mass leaves the simulation in four ways: (1) Worms utilize mass for metabolic maintenance. (2) Worms utilize mass when they grow or generate eggs, since these processes may be less than 100% efficient. (3) Worms transition to death, and their mass leaves the simulation. (4) Bacteria are removed by culling, and their mass leaves the simulation. Thus, the fate of all the mass that enters the simulation can be determined.

Supplementary Section 4. Using a training data set to establish certain parameters.

To develop a realistic simulation of the laboratory ecosystem, we measured the traits of individual worms whenever it was feasible. However, some traits could not be measured, including “cost of living”, which we define as the percent of an individual’s mass that is consumed at each time step to maintain metabolism, and “metabolic efficiency”, which we define as the percent of ingested bacteria that is converted to growth mass or egg mass. To estimate these values, we used the data from one laboratory ecosystem experiment as a training set; we compared the data from replicate 2a of the laboratory ecosystem (Figure 3A,B, Extended Data Figure 2B) to simulations with different values of “cost of living” and “metabolic efficiency.” When we used a value of 3.5%/3h for “cost of living” and 85% for “metabolic efficiency”, there was a good correspondence between the average number of worms in replicate 2a and the average number of worms in the simulation. We used these values for subsequent simulations, and replicate 2a was the only laboratory ecosystem data that was used as a training set.

Supplementary Table 17. Equations and transition rules for the simulation.

worm behavior ¹	Equation ²	Parameters ³	Comment
larva and adult growth	$\Delta m = Km(1 - bm)$ for one time step	$K = 1.78 * \tanh(2.13 * food)$ $b = 1.30 * 10^{-4} - 2.49 * 10^{-4} / food$	Logistic growth, continuous between larvae and adults. m is mass in ng. t is time in days. food is in mg/ml. b is in reciprocal ng.
adult egg laying	$\frac{eggs}{day} = Mx^n \exp(-x/x_o)$	$M = 17.33 * x^{-0.166} + 30.08$ $n = -1.867 * x^{-0.299} + 5.908$ $x_o = 0.233 * x^{-0.762} + 0.581$	x is adult age (days).
larva and adult feeding	$\frac{1}{consumption} = \frac{1}{appetite} + \frac{1}{portion}$	$portion = food * \frac{appetite}{\sum(all\ appetites)}$	Adding the reciprocals assures that the food eaten will always be less than appetite and less than portion.
larva appetite	$appetite = \Delta m / \varepsilon$	Δm is defined above ε = efficiency is an input parameter	ε = is set to unity in our model
adult appetite	$\frac{\Delta m}{\varepsilon} + \frac{eggs}{day} * \frac{1}{8} * \frac{eggmass}{\varepsilon}$		1/8 converts days to time steps
larva transition to dauer	$probability\ of\ dauer\ = 0.5 \exp(-\frac{[avg\ food]}{2.5E5})$	Probability is for one-time period. Average food is the total amount of food in the medium averaged over the present time period and the start of the previous time period.	Larva is only eligible to dauer while its mass is between 137 ng and 456 ng.

dauer transition to larva	$prob = .0000324 * \sqrt{(\text{avg food})^{\wedge}}$	Probability is for one-time period. Average food is the total amount of food in the medium averaged over the present time period and the start of the previous time period.	When a dauer transitions to a larva, the larva has the same mass and age as when it entered dauer.
dauer starvation	$probability = \frac{\exp(\frac{age}{800} - 1)}{(1 + \exp(\frac{age}{800} - 1))}$	Probability is for one-time period. Age is number of periods that the dauer has been a dauer. 800 is the starvation time set in all experiments.	A low number of dauers starves every time step dependent on their age as a dauer.
parlad releases dauers	10 time periods (30h), number of dauers = $\epsilon m / \text{dauer mass}$	$\epsilon = 0.667$ dauer mass = 228 ng	The whole of the parlad's biomass is converted to dauers with an efficiency ϵ .
adult mortality per unit time (die of old age)	$\frac{1}{A} (\exp(\frac{x}{\tau}) - 1)$	$A = 168(e^4 - 1)$ $\tau = 35.7$	Gompertz mortality Time measured in 3h periods. x is adult age.

¹Worms feed on bacteria, grow, lay eggs, release dauers, transition to a new stage, or transition to death.

²Equations were created to describe worm behaviors.

³Equations include parameters whose values were determined to use these equations.

Supplementary Table 18. Initialization of environment and agents in the simulation.

Component ¹	Environment/agent ¹	unit	user programmable input values ²	Description ³
bacteria	environment	mass in mg	5 or 10	
egg	agent	number	0, 100 or 250	65 ng; -1 to -5 time steps
larva	agent	number	0, 250, or 1000	228 ng; 0 to 5 time steps
dauer	agent	number	0, 100, 250, or 1000	228 ng; 5-15 time steps

¹Bacteria are considered part of the environment, whereas egg, larva and dauer are agents.

²All of these inputs and no others were used in this study. Only one input value was used per simulation experiment.

³Mass of worms (ng), and age of the worms in time steps. Eggs are laid at time step -5, and eggs hatch at time step 0.

Supplementary Table 19. Maintenance of environment and agents in the simulation.

Variable ¹	unit	user programmable input values ²	Simulation duration ³
bacterial addition interval	hours	24 or 48	100 day
bacterial addition amount	mg	5 or 10	100 day
fixed bacteria concentration ⁴	mg/ml	0.04-16	one worm generation - only used to model a constant food environment
culling interval	hours	24 or 48	100 day
culling amount (all stages and bacteria)	percent	0, 5, or 10	100 day
culling larva (stage-specific)	percent	0-90	100 day
culling dauer (stage-specific)	percent	0-90	100 day
culling adult (stage-specific)	percent	0-40	100 day
culling eggs (stage-specific)	percent	0-90	100 day

¹The amount and interval of bacteria addition and culling are specified for each simulation run.

²All of these inputs and no others were used in this study. Only one input value was used per simulation experiment.

³Most simulations had a duration of 100 days, but simulations with a constant concentration of bacteria had a duration of one worm generation.

⁴A fixed concentration of bacteria was used in simulations that compared virtual worms to live worms cultured in a fixed concentration of bacteria in the laboratory (Figure 2, Supplementary Figure 2-7).

Supplementary Table 20. Agent traits with a user programmable input value in the simulation.

worm node ¹	Trait ²	unit	user programmable input values ³	Description	Determined ⁴
adult	maximum adult life span	days	25, 40, or 60	This number scales the Gompertz function for senescent death.	laboratory measurement for wild type - 40 days.
dauer	bacteria concentration triggering larva transition to dauer	mg/mL	<0.05 or <0.000002	if this condition is true larva are eligible to transition to starve or dauer	$wt(l>d)$
dauer	starvation time	days	100 or 0.125	probability of dauer starvation increases if dauer age is close to starvation time	$wt(d>s)$
adult/parlad	bacteria concentration triggering adult transition to parlad	mg/mL	<0.0005 or 0	Bacteria concentration averaged over two time periods that induces adult transition to parlad.	$wt(a>p)$

¹The worm stage affected by the user programmable input value.

²The property or trait of the agent specified by the user programmable input value, in this case maximum adult lifespan

³All of these inputs and no others were used in this study. Only one input value was used per simulation experiment.

⁴User programmable input values were determined by laboratory measurement or estimated. The maximum adult lifespan of wild-type worms was measured to be ~40 days in the laboratory, and values of 25 and 60 days are theoretical maximum lifespans that do not correspond to wild type.

Supplementary Table 21. Agent traits with a fixed input value in the simulation.

	worm node ¹	Trait ²	unit	Fixed input value ³	description	Transition ⁴	Determined ⁵
1	egg/adult	egg mass	ng	65	mass of every egg in the simulation	wt(a>e)	laboratory measurement
2	egg	duration of the egg stage	hours	15	Time before an egg hatches into a larva	wt(e>l)	laboratory measurement
3 ⁶	larva	bacteria concentration triggering larva transition to starve or dauer	mg/mL	<0.05	if this condition is true larva are eligible to transition to starve or dauer	wt(l>s) wt(l>d)	estimate
4	larva	duration of low level of bacterial food that triggers larva transition to starve or dauer	hours	6	if this condition is true, larva are eligible to transition to starve or dauer	wt(l>s) wt(l>d)	estimate
5	larva	probability of larva transition to starvation	percent	50%	This trait ensures that not all larva starve at the same time and ensures variation if condition is true in rows 3 and 6. Stochastic.	wt(l>s)	estimate based on training set
6	larva	larva to dauer transition mass range	ng	137-456	larva can only transition to dauer within this mass range.	wt(l>d)	estimate
7	larva/dauer	mass of dauer derived from larva	ng	137-456	Dauer mass equals larva mass before transition, which must be in this range	wt(l>d)	estimate
8	larva/adult	Minimum age for larva to adult transition	hours	160	Larva cannot transition to adult before this age, irrespective of mass.	wt(l>a)	laboratory measurement
9	larva/adult	mass range for larva to adult transition	ng	800-3200	Larva cannot transition to adult unless they achieve this minimum mass.	wt(l>a)	laboratory measurement

10	larva/adult	metabolic efficiency	percent	85%	Percent of ingested bacteria mass converted into worm growth and eggs.		estimate based on training set
11	larva/adult	cost of living	percent/hours	3.5%/3h	Mass consumed in metabolic processes (for example, locomotion).		estimate based on training set
12 ⁷	adult	maximum life span	days	40	This number scales the Gompertz function for senescent death.	wt(a>o)	laboratory measurement (see Supplementary Table 21)
13	adult	probability of dying of old age prior maximum adult lifespan	number	4	Another Gompertz parameter. Lower numbers correspond to an S-shaped survival curve, higher numbers to a square curve in which all adults die in a narrow window.	wt(a>o)	laboratory measurement
14	adult/parlad	duration of low level of bacterial food that triggers adult to parlad transition	hours	6	Number of time periods on average that it takes for an individual adult to transition to parlad when bacterial food concentration is below the parlad food threshold.	wt(a>p)	estimate
15 ⁸	adult/parlad	bacteria concentration triggering adult transition to parlad	mg/mL	<0.0005	Bacteria concentration averaged over two time periods that induces adult transition to parlad.	wt(a>p)	estimate
16	parlad	duration of the parlad stage	hours	30	Time before a parlad bursts and releases dauers.	wt(p>d)	estimate

17	parlad/dauer	Mass of dauer derived from parlad	ng	228	All dauer derived from parlad have this mass.	wt(p>d)	estimate
18	parlad/dauer	number of dauer generated by parlad	number	mass parlad/mass dauer ⁵ ε	All parlad biomass is converted to dauer with an efficiency $\epsilon=0.66$ rounded to the nearest whole number	wt(p>d)	estimate
19	dauer	bacteria concentration triggering dauer transition to larva	mg/mL	> 0.05	Bacteria concentration that scales individual propensity for dauer to larva transitions.	wt(d>l)	estimate
20	dauer	probability of dauer transition to larva	probability	3.24E-5	Probability per time step of a dauer transitioning to a larva when bacterial food concentration is above the dauer food threshold. Stochastic.	wt(d>l)	laboratory measurement
21 ⁹	dauer	starvation time	days	100	probability of dauer starvation increases if dauer age is close to starvation time	wt(d>s)	

¹The worm stage(s) affected by the fixed input value.

²The property or trait of the agent specified by the fixed input value.

³These input values and no others were used in this study, except for maximum adult lifespan as described in Supplementary Table 21. Only one input value was used per simulation experiment.

⁴Worm transitions affected by the fixed input value.

⁵Fixed input values were determined by laboratory measurement or estimated. In some cases, estimates were based on a training data set (see Supplementary Section 4).

⁶Bacteria concentration triggering larva transition to dauer was fixed to <0.05 mg. In some simulations, we analyzed virtual worms (*in silico* mutants) with bacteria concentration triggering larva transition to dauer <0.000002.

⁷Maximum adult lifespan was measured to be 40 days. In some simulations, we analyzed virtual worms (*in silico* mutants) with 25 and 60-day maximum adult lifespans.

⁸Bacteria concentration triggering adult transition to parlad was fixed to <0.0005 mg/mL. In some simulations, we analyzed virtual worms (*in silico* mutants) with 0 mg/mL bacteria concentration triggering adult transition to parlad.

⁹Dauer starvation time was fixed to 100 days according measurements. In some simulations, we analyzed virtual worms (*in silico* mutants) with 0.125 days dauer starvation time.

Supplementary Literature:

1. Lahdenperä, M., Mar, K. U. & Lummaa, V. Reproductive cessation and post-reproductive lifespan in Asian elephants and pre-industrial humans. *Front. Zool.* **11**, 1–14 (2014).
2. Brittain, J. E. Biology of Mayflies. *Annu. Rev. Entomol.* **27**, 119–147 (1982).
3. Burks, B. D. The Mayflies, or Ephemeroptera, of Illinois. *Bulletin* **26**, 1–203 (1953).
4. Trebilco, R., Baum, J. K., Salomon, A. K. & Dulvy, N. K. Ecosystem ecology: Size-based constraints on the pyramids of life. *Trends Ecol. Evol.* **28**, 423–431 (2013).
5. McNaughton, S. J. Ecology of a Grazing Ecosystem : The Serengeti. *Soc. Ecol. Monogr. Ecol.* **55**, 259–294 (2018).
6. Odum, E. P. & Barret, G. W. Fundamentals of Ecology. *J. Range Manag.* **12**, 313 (1959).
7. A.J. Willis. The Ecosystem : An Evolving Concept Viewed Historically. *Funct. Ecol.* **11**, 268–271 (1997).
8. Evans, F. C. Ecosystem as the Basic Unit in Ecology. **123**, 1127–1128 (1956).
9. Petrascheck, M., Ye, X. & Buck, L. B. An antidepressant that extends lifespan in adult *Caenorhabditis elegans*. *Nature* **450**, 553–556 (2007).
10. Grimm, V. *et al.* The ODD protocol: A review and first update. *Ecol. Model.* **221**, 2760–2768 (2010).
11. Grimm, V. *et al.* The ODD protocol for describing agent-based and other simulation models: A second update to improve clarity, replication, and structural realism. *Jasss* **23**, (2020).
12. Wilensky, U. & Rand, W. An introduction to agent-based modeling: modeling natural, social, and engineered complex systems with NetLogo. *MIT Press* (2015).
13. Golden, J. W. & Riddle, D. L. The *Caenorhabditis elegans* dauer larva: Developmental effects of pheromone, food, and temperature. *Dev. Biol.* **102**, 368–378 (1984).
14. Pickett, C. L. & Kornfeld, K. Age-related degeneration of the egg-laying system promotes matricidal hatching in *Caenorhabditis elegans*. *Aging Cell* **12**, 544–553 (2013).
15. Sawin, E. R., Ranganathan, R. & Horvitz, H. R. *C. elegans* locomotory rate is modulated by the environment through a dopaminergic pathway and by experience through a serotonergic pathway. *Neuron* **26**, 619–631 (2000).
16. Chen, J. & Caswell-Chen, E. P. Facultative vivipary is a life-history trait in *Caenorhabditis elegans*. *J. Nematol.* **36**, 107–113 (2004).

Supplementary Section 5:

KK Acknowledgments: Yesterday a child came out to wander, caught a dragonfly inside a jar. K.K. is deeply grateful to many people who transformed a vision into reality. My parents, Rosalind and Stuart Kornfeld, gave me the freedom to be outdoors and fostered my independence. I wandered the fields and creeks, catching butterflies and watching birds, connecting to nature and its rhythms. They also brought me to the lab, a special place to explore the mysteries of nature. A long, long, time ago, I can still remember how that immature bald eagle made me wonder – why so many years until the white head and eggs? Why does the apex predator display reproductive restraint, and how does this relate to reproductive aging? To my dear friend Jonathon Losos, my partner in crime, who invited me to see the eagle - through chess club, bridge and debate, the St Louis Zoo, north woods of Camp Nebagamon, Chiricahue Mountains, Big Bend, and the Great Smokies, you were bold and brilliant and an inspiration. Let this be our new beginning. To Cheng Huang, Stacie Hughes, Kim Eason, and Jim Collins, your amazing discoveries of aging set the stage. Long live the optimal progeny number theory. To Brinda Armstead, my sincerest thanks for the leap of faith in 2008 to start the laboratory ecosystem. To Chris Pickett for your steady hand in those early days. To Luke Schneider, who worked with Brinda and is still here today, it could not have happened without you my friend. The computer simulation was the hardest part. It was long ago and far away when Larry Taber informed me the idea had a name: agent-based model. To Wei Tao, for the first attempt at NetLogo, you made me a believer. To Lu Chen, James Tan, Alex Sigala, Zuzana Kocsisova, Asa Earnest, and He Jin who kept the dream alive. To Josh Mitteldorf, who wrote the code, I have learned so much. I treasure our friendship and collaboration and your wisdom and skill. To Andrea Scharf, who got the job done. Your persistence, energy and skill made it a reality – it was the hardest nut to crack, and I watched in awe. To Andrea's helpers - Francesca Sanchez, Brian Brady, Natasha Ram, Gabe DiAntonio, and Orion Kornfeld – we needed each of you, and a pandemic couldn't stop us. To Andrea Wilson, words cannot

express my gratitude. Every step of the way your wisdom and perspective made it possible. To Jerry Garcia, Robert Hunter and the Grateful Dead for inspiration - the seeds that were silent all burst into bloom, and decay. Thanks to all the members of the Kornfeld lab that made it happen, because our collaborative efforts are our greatest achievements. To Joni Mitchell for expressing the essence - we're captive on the carousel of time. We can't return, we can only look behind, from where we came, and go round and round and round in the circle game.