## Appendix 1. Life cycles competition

In the result of population dynamics described above, some life cycles become more abundant, while others go extinct. The outcome of this life cycle competition is independent on he resource limitation parameter (K) and is exactly the same as in the linear model without resource limitation at all ( $K \rightarrow \infty$ ).

<sup>6</sup> To show this, consider the whole population describe by values  $x_i^{\kappa}(t)$  - the number of <sup>7</sup> groups of size *i* in the lineage executing life cycle  $\kappa$ . We can decompose this value into a <sup>8</sup> form

$$x_i^{\kappa}(t) = X(t) f^{\kappa}(t) \rho_i^{\kappa}(t), \tag{1}$$

where X(t) is the total number of units in a population,  $f^{\kappa}(t)$  is the fraction of units following the life cycle  $\kappa$ , and  $\rho_i^{\kappa}(t)$  is the fraction of them, which have a size *i*. Naturally,

$$\sum_{\kappa} f^{\kappa}(t) = 1, \tag{2}$$

13 
$$\sum_{i} \rho_{i}^{\kappa}(t) = 1.$$
 (3)

The quantity  $f^{\kappa}(t)$  characterizes the evolutionary success of a life cycle, and we are generally interested in its dynamics.

In Eqs. (3), the terms responsible for units growth, death, and fragmentation are linear with respect to  $x_i$ , and therefore, these equations can be represented as

$$\frac{d}{dt}x_i = \sum_j A_{ij}x_j - \frac{1}{K}Xx_i,\tag{4}$$

where  $A_{ij}$  is some constant matrix. In particular, this equation is valid independently for each life cycle  $\kappa$ .

<sup>23</sup> Combining Eqs. (4) and (1), we get

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24 25

$$\frac{d}{dt}(Xf^{\kappa}\rho_{i}^{\kappa}) = Xf^{\kappa}\sum_{j}A_{ij}\rho_{j}^{\kappa} - \frac{1}{K}X^{2}f^{\kappa}\rho_{i}^{\kappa}.$$
(5)

Summation over all units sizes i in Eq. (5) results with

$$\frac{d}{dt}(Xf^{\kappa}) = Xf^{\kappa}\sum_{i,j}A_{ij}\rho_j^{\kappa} - \frac{1}{K}X^2f^{\kappa}.$$
(6)

- <sup>29</sup> And after rearranging the terms
- 30 31

 $\frac{d}{dt}f^{\kappa} = f^{\kappa}\sum_{i,j}A_{ij}\rho_j^{\kappa} - \frac{1}{K}Xf^{\kappa} - f^{\kappa}\frac{1}{X}\frac{d}{dt}X.$ (7)

<sup>32</sup> There, summation over all life cycles provides

$$\frac{1}{X}\frac{d}{dt}X = \sum_{i,j,\kappa} A_{ij}\rho_j^{\kappa}f^{\kappa} - \frac{1}{K}X.$$
(8)

<sup>35</sup> Plugging Eq. (8) back into Eq. (7), we finally obtain

$$\frac{d}{dt}f^{\kappa} = f^{\kappa}\left(\sum_{i,j}A_{ij}\rho_{j}^{\kappa} - \sum_{i,j,\mu}A_{ij}\rho^{\mu}f^{\mu}\right).$$
(9)

The dynamics of life cycles competition explicitly given by Eq. (9) is independent on the severity of the resources limitation K and the total number of units X. The competition of life cycles has the same outcome in the model without resource competition at all  $(K \to \infty)$ .

## Appendix 2. Linear model of life cycles evolution

<sup>2</sup> Without resource competition, the population dynamics is governed by a system of equations

 $\frac{d}{dt}x_1 = -b_1x_1 - d_1x_1 + \pi_1(\kappa)mb'_m x_m$ (1a)

$$5 \qquad \frac{d}{dt}x_i = -ib_i x_i + (i-1)b_{i-1}x_{i-1} - d_i x_i + \pi_i(\kappa)mb'_m x_m \quad \text{for} \quad 1 < i < m$$
(1b)

$$\frac{d}{dt}x_m = -mb'_m x_m + (m-1)b_{m-1}x_{m-1} - d'_m x_m + \pi_m(\kappa)mb'_m x_m.$$
(1c)

<sup>8</sup> The equation system Eq. (1) is linear with respect to  $x_i$ . Thus, it can be written as:

$$\frac{d}{dt}\mathbf{x} = A\mathbf{x},\tag{2}$$

10 where  $\mathbf{x} = (x_1, x_2, \cdots, x_m)^T$  and the matrix A is

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11

$$A = \begin{pmatrix} -b_1 - d_1 & 0 & 0 & \cdots & \pi_1(\kappa)mb'_m \\ b_1 & -2b_2 - d_2 & 0 & \cdots & \pi_2(\kappa)mb'_m \\ 0 & 2b_2 & -3b_3 - d_3 & \cdots & \pi_3(\kappa)mb'_m \\ 0 & 0 & 3b_3 & \cdots & \pi_4(\kappa)mb'_m \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & \pi_m(\kappa)mb'_m - mb'_m - d'_m \end{pmatrix}$$
(3)

In the long run, the solution of Eq. (2) converges to that of an exponentially growing population with a stable distribution, i.e.,

$$\lim_{t \to \infty} \mathbf{x}(t) = e^{\lambda t} \mathbf{w}.$$
 (4)

The leading eigenvalue  $\lambda$  gives the total population growth rate, and its associated right eigenvector  $\mathbf{w} = (w_1, \dots, w_m)$  gives the stable distribution of unit sizes.

The leading eigenvalue determines the evolutionary success of a population. In the competition of populations utilizing different life cycles (and hence different  $\lambda$ ), each of them will grow independently of the others. Eventually, the population with the largest growth rate will outcompete the others. Thus, natural selection would promote the life cycle that provides the largest  $\lambda$ . We call this the evolutionarily optimal life cycle.

## Appendix 3.

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 $\overline{i=1}$ 

## <sup>2</sup> Characteristic equation for an arbitrary life cycle

<sup>3</sup> Consider a life cycle in which the number of cells in a unit increases until the maturity size *m* is reached and once the next cell is born, a unit fragments according to a partition κ of *j'* ≤ *m* + 1. The corresponding projection matrix is an *m* × *m* matrix of the form

<sup>9</sup> The population growth rate is given by the leading eigenvalue  $\lambda_1$  of *A*, i.e., the largest solution <sup>10</sup> of the characteristic equation

$$\det\left(A - \lambda \mathbf{I}\right) = 0. \tag{2}$$

By using a Laplace expansion along the last column of  $A - \lambda \mathbf{I}$ , we can rewrite the left hand side of the above expression (i.e., the characteristic polynomial of A) as

$$\det (A - \lambda \mathbf{I}) = \sum_{i=1}^{m-1} (-1)^{i+m} m b'_m \pi_i(\kappa) M_{i,m} + (-1)^{2m} (m b'_m \pi_m(\kappa) - m b'_m - d'_m - \lambda) M_{m,m}$$

$$= \sum_{i=1}^m (-1)^{i+m} m b'_m \pi_i(\kappa) M_{i,m} - (m b'_m + d'_m + \lambda) M_{m,m}$$
(3)

<sup>17</sup> where  $M_{i,m}$  is the (i,m) minor of  $A - \lambda I$ . For all i = 1, ..., m, the minor  $M_{i,m}$  is the <sup>18</sup> determinant of a block diagonal matrix, and hence equal to the product of the determinants of <sup>19</sup> the diagonal blocks. Moreover, each diagonal block is either a lower triangular or an upper <sup>20</sup> triangular matrix, whose determinant is given by the product of the elements in their main

diagonals. We can then write 

$$M_{i,m} = \prod_{j=1}^{i-1} \left( -jb_j - d_j - \lambda \right) \prod_{j=i}^{m-1} jb_j.$$
(4)

Substituting Eqs. (3) and (4) into Eq. (2), switching the order of the two terms and simplify-

ing, we obtain 

25 
$$-(-1)^{m-1}(mb'_m+d'_m+\lambda)\prod_{j=1}^{m-1}(jb_j+d_j+\lambda)$$

+ 
$$(-1)^{m-1} \sum_{i=1}^{m} mb'_m \pi_i(\kappa) \prod_{j=1}^{i-1} (jb_j + d_j + \lambda) \prod_{j=i}^{m-1} jb_j = 0.$$

Dividing both sides by 

29 
$$(-1)^m \prod_{j=1}^m jb_j,$$

we get 

$$\frac{mb'_m + d'_m + \lambda}{mb_m} \prod_{j=1}^{m-1} \left(1 + \frac{d_j + \lambda}{jb_j}\right)$$

$$-\sum_{i=1}^m \frac{b'_m}{b_m} \pi_i(\kappa) \prod_{j=1}^{i-1} \left(1 + \frac{d_j + \lambda}{jb_j}\right) = 0.$$

We rewrite the factor in front of the product in the first line as 

$$\frac{mb'_m + d'_m + \lambda}{mb_m} = \left(1 + \frac{d_m + \lambda}{mb_m}\right) + \frac{m(b'_m - b_m) + d'_m - d_m}{mb_m}.$$

Thus, 

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$$\prod_{j=1}^{m} \left( 1 + \frac{d_j + \lambda}{jb_j} \right) + \frac{m(b'_m - b_m) + d'_m - d_m}{mb_m} \prod_{j=1}^{m-1} \left( 1 + \frac{d_j + \lambda}{jb_j} \right)$$
39 
$$- \frac{b'_m}{b_m} \sum_{i=1}^{m} \pi_i(\kappa) \prod_{j=1}^{i-1} \left( 1 + \frac{d_j + \lambda}{jb_j} \right) = 0.$$

Simplifying this, we finally obtain that the characteristic equation (2) can be written as

$$F_{m+1}(\lambda) + \Delta_m F_m(\lambda) - \frac{b'_m}{b_m} \sum_{i=1}^m \pi_i(\kappa) F_i(\lambda) = 0,$$
(5)

where 

$$F_i(\lambda) = \prod_{j=1}^{i-1} \left( 1 + \frac{d_j + \lambda}{jb_j} \right).$$
(6)

and  $\Delta_{i} = \frac{i(b'_{i} - b_{i}) + d'_{i} - d_{i}}{ib_{i}}.$ (7) Note that two transformations preserve Eq. (5):

$$\underset{49}{\overset{48}{}} \qquad \qquad d_i \to d_i - r, \qquad d' \to d' - r, \qquad \lambda_1 \to \lambda_1 + r, \qquad r \le \min(\mathbf{d}),$$
(8)

50 and

51  $\mathbf{d} \to s\mathbf{d}, \quad \mathbf{b} \to s\mathbf{b},$ 52  $b' \to sb', \quad d' \to sd', \quad \lambda_1 \to s\lambda_1, \quad s > 0.$ 

These transformations allow us to set  $b_1 = 1$  and  $\min(\mathbf{d}) = 0$  without loss of generality.

## **<sup>55</sup>** Forbidden fragmentation modes

For any environment, for any combination of the fragmentation delay, risk and fixed loss, the fragmentation mode having two different subsets of offspring with the same combined size is dominated. To prove this, we use approach similar to one used in Appendix E in [1]. Consider positive integers m, j, k such that  $m + 1 \ge 2j + k$ , two partitions of j,  $\tau_1$  and  $\tau_2$ , such that  $\tau_1 \ne \tau_2$ , and an arbitrary partition  $\phi$  of k, and the following three deterministic fragmentation modes:

1.  $\kappa_1 = \tau_1 + \tau_2 + \phi$  - the partition of  $2j + k \le m + 1$ , whereby a unit fragments upon the increment of size from m to m + 1 into a number of offspring given by partitions  $\tau_1$ ,  $\tau_2$ , and  $\phi$ .

<sup>65</sup> 2.  $\kappa_2 = \tau_1 + \tau_1 + \phi$  – the partition of  $2j + k \le m + 1$ , whereby a unit fragments upon the <sup>66</sup> increment of size from m to m + 1 into a number of offspring given by two partitions <sup>67</sup>  $\tau_1$  and one partition  $\phi$ .

68 3.  $\kappa_3 = \tau_2 + \tau_2 + \phi$  – the partition of  $2j + k \le m + 1$ , whereby a unit fragments upon the 69 increment of size from m to m + 1 into a number of offspring given by two partitions 70  $\tau_2$  and one partition  $\phi$ . <sup>71</sup> Denoting by  $\lambda(\kappa_i)$  the leading eigenvalue of the projection matrix induced by fragmentation <sup>72</sup> mode  $\kappa_i$ , we can show that, for any environment, either  $\lambda(\kappa_1) \leq \lambda(\kappa_2)$  or  $\lambda(\kappa_1) \leq \lambda(\kappa_3)$ <sup>73</sup> holds. Thus, a fragmentation mode with two different subsets of offspring with the same <sup>74</sup> combined size is dominated by a mode where one of these subsets repeats twice, while the <sup>75</sup> other one is not present.

To prove the statement above, let us define the polynomial  $p_i(\lambda)$  as the left hand side of Eq. (5) with  $\kappa = \kappa_i$ , so that  $\lambda(\kappa_i)$  is the largest root of  $p_i(\lambda)$ . We obtain

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$$p_{1}(\lambda) = F_{m+1}(\lambda) + \Delta_{m}F_{m}(\lambda) - \frac{b'_{m}}{b_{m}} \left( \sum_{i=1}^{m} \pi_{i}(\tau_{1})F_{i}(\lambda) + \sum_{i=1}^{m} \pi_{i}(\tau_{2})F_{i}(\lambda) + \sum_{i=1}^{m} \pi_{i}(\phi)F_{i}(\lambda) \right)$$
(9a)

79 
$$p_2(\lambda) = F_{m+1}(\lambda) + \Delta_m F_m(\lambda) - \frac{b'_m}{b_m} \left( 2\sum_{i=1}^m \pi_i(\tau_1) F_i(\lambda) + \sum_{i=1}^m \pi_i(\phi) F_i(\lambda) \right)$$
 (9b)

80 
$$p_3(\lambda) = F_{m+1}(\lambda) + \Delta_m F_m(\lambda) - \frac{b'_m}{b_m} \left( 2\sum_{i=1}^m \pi_i(\tau_2) F_i(\lambda) + \sum_{i=1}^m \pi_i(\phi) F_i(\lambda) \right)$$
 (9c)  
81

<sup>82</sup> These polynomials satisfy the following two properties. First,

$$\lim_{\lambda \to \infty} p_i(\lambda) = \infty, \tag{10}$$

as the leading coefficient of the left hand side of (5) is given by  $(b_1 \cdot b_2 \cdot \ldots \cdot b_m m!)^{-1}$ , which is always positive. Second,

$$p_1(\lambda) = \frac{p_2(\lambda) + p_3(\lambda)}{2}.$$
(11)

Since  $\lambda(\kappa_1)$  is a root of  $p_1(\lambda)$ , evaluating Eq. (11) at  $\lambda(\kappa_1)$  leads to

$$p_2(\lambda(\kappa_1)) = -p_3(\lambda(\kappa_1)).$$

<sup>89</sup> Hence, one of the following three scenarios is satisfied:

90 (i) 
$$p_2(\lambda(\kappa_1)) < 0 < p_3(\lambda(\kappa_1)),$$

86

91 (ii) 
$$p_2(\lambda(\kappa_1)) > 0 > p_3(\lambda(\kappa_1))$$
, of

92 (iii) 
$$p_2(\lambda(\kappa_1)) = p_3(\lambda(\kappa_1)) = 0.$$

If  $p_2(\lambda(\kappa_1)) < 0 < p_3(\lambda(\kappa_1))$  due to Eq. (10) and Bolzano's theorem (if a continuous func-

 $_{
m 94}~~$  tion has values of opposite sign inside an interval, then it has a root in that interval),  $p_2(\lambda)$  has

a root between  $\lambda(\kappa_1)$  and  $\infty$ . Therefore,  $\lambda(\kappa_1) \leq \lambda(\kappa_2)$  holds, i.e. the largest root of  $p_2(\lambda)$  is larger than the largest root of  $p_1(\lambda)$ . Next, let us focus on (ii): If  $p_2(\lambda(\kappa_1)) > 0 > p_3(\lambda(\kappa_1))$ , then  $\lambda(\kappa_1) \leq \lambda(\kappa_3)$  holds. Finally, if  $p_2(\lambda(\kappa_1)) = p_3(\lambda(\kappa_1)) = 0$ , then both  $\lambda(\kappa_1) \leq \lambda(\kappa_2)$ and  $\lambda(\kappa_1) \leq \lambda(\kappa_3)$  hold.

We conclude that either  $\lambda(\kappa_1) \leq \lambda(\kappa_2)$  or  $\lambda(\kappa_1) \leq \lambda(\kappa_3)$  must hold. Thus, the life cycle corresponding to  $\kappa_1$  can never lead to the highest growth rate.

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- <sup>103</sup> of life cycles. *PLoS Computational Biology*, 13(11):e1005860, 2017.

## Appendix 4. Random environments

#### 2 Uncorrelated random environments

We numerically investigate the distribution of optimal life cycles on two sets of environments:
random environments and random detrimental environments, which strongly disfavour multicellular units. Both sets are explored by 10000 environments generated only once and then
used to assess all three scenarios: delay, risk, and loss.

In the set of random environments, each element of the division and death rates vector (b and d) was sampled independently from the uniform distribution U(0, 1).

#### 9 Random detrimental environments

To construct an unbiased set of random detrimental environments we used a method adopted 10 from [1]. For each environment, we initially sampled two sequences of n = 19 random 11 numbers from the uniform distribution U(0,1). Then, the first sequence has been sorted 12 in descending order to form the vector of the division rates b and the second sequence has 13 been sorted in ascending order to form the vector of death rates d. Thus, in all detrimental 14 environments, the values of division rates monotonically decreased with the unit size, while 15 the values of death rates monotonically increased. Therefore, life cycles that fragment at 16 large sizes only are strongly disfavoured. 17

#### **18** Random beneficial environments

The set of random beneficial environments was constructed in a similar way. There, for each environment, we first sampled two sequences of n = 19 random numbers from the uniform distribution U(0, 1). Then, the first sequence has been sorted in ascending order to form the vector of the increasing division rates b and the second sequence has been sorted in descending order to form the vector of decreasing death rates d. In the result, the largest possible size is the most productive and the most defended state of a multicellular unit.

### **Random unimodal environments**

To construct the set of random unimodal environments, we again started with two sorted 26 sequences of random numbers from the uniform distribution U(0,1). Then, to construct the 27 division rates vector, the largest value of the first sequence was assigned to the optimal size of 28 10 cells. The second largest value was randomly assigned either to the position on the left (9 29 cells) or the right (11 cells). Then, the next largest value was randomly assigned to either of 30 two free slots closest to 10-th position. Hence, the vector of division rates has the maximum 31 at 10 cells and monotonically decreases in both directions away from it. The vector of death 32 rates was constructed in the similar way, with the minimum of death rate being at the optimal 33 size of 10 cells. 34

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# Appendix 5. Binary fragmentation and (nearly) equal split are overrepresented in beneficial and unimodal environments.

Besides environments with uncorrelated random values of birth and death rates (see Fig. 4
in the main text) and detrimental environments (see Fig. 5 in the main text), we investigated
beneficial and unimodal environments. Both demonstrated patterns qualitatively similar to
the environments with uncorrelated random values, see Figs. 1 and 2.



Figure 1: Binary fragmentation and (nearly) equal split are overrepresented in beneficial environments. In this case, fragmentation always occurs at the largest possible size. The fractions of each of four classes of life cycles under (A) delay, (B) risk, and (C) loss fragmentation costs.



Figure 2: Binary fragmentation and (nearly) equal split are overrepresented in unimodal environments. The fractions of each of four classes of life cycles under (A) delay, (B) risk, and (C) loss fragmentation costs.

## Appendix 6. Only deterministic fragmentation modes can be evolutionarily optimal under any environment

Following [2], the state of the population can be described by the vector  $\mathbf{x}$ , where  $x_i$  denotes the abundance of units of size *i*. All processes changing the state vector  $\mathbf{x}$  – birth, death and fragmentation – occur with a constant rate. Thus, the dynamics of the population state can be described by a set of linear differential equations or, equivalently, by a matrix differential quation

$$\dot{\mathbf{x}} = A\mathbf{x},\tag{1}$$

8

18

<sup>9</sup> where A is a projection matrix defined by demographics of the population [1]. An element <sup>10</sup>  $a_{i,j}$  of the projection matrix describes the rate of change of the number of units of size i<sup>11</sup> caused by processes occurring with units of size j.

To construct the projection matrix elements, consider units of a certain size j. We denote by  $q_{j,\kappa}$  the probability that upon the increase in size from j to j + 1, the unit will fragment by a partition  $\kappa$  of  $j' \leq j + 1$  (where the " $\leq$ " indicates that cells can be lost upon fragmentation). Among these partitions we distinguish the trivial partition of j + 1 that corresponds to the cell division without fragmentation; we denote this by  $q_{j,(j+1)}$ . The combined probability of all outcomes is equal to one:

$$\sum_{\kappa} q_{j,\kappa} = 1. \tag{2}$$

For deterministic life cycles, only one partition occurs in all cell clusters in a population. Thus, for unit sizes j up to maturity size m, the trivial partition occurs with probability one  $(q_{j,(j+1)} = 1)$ , while all other partitions have zero probability. Once a cell divides in a cluster that reached the maturity size, a certain non-trivial partition of  $j' \leq m + 1$  occurs with probability one. In a stochastic life cycle, more than one partition has non-zero probability at least at one unit size.

To show that stochastic life cycles are dominated by deterministic ones, we construct the projection matrix for an arbitrary stochastic life cycle. The number of cells in a unit increases by one cell at a time, thus no process can increase the size of a cluster by more than one unit at once, so  $a_{i,j} = 0$  for all i > j + 1. Thus, the projection matrix may contain non-zero elements only in the upper right triangle (emergence of smaller units during fragmentation), on the main diagonal (fragmentation, cell division and death of units), and on the first lower subdiagonal (increment of a unit size due to a cell division).

The first lower subdiagonal describes the rate of emergence of new larger units due to cell division without fragmentation. These rates are equal to the product of the number of cells in a unit, their division rate, and the probability the fragmentation does not occur:

$$a_{j+1,j} = jb_j q_{j,(j+1)}.$$
 (3)

The upper right triangle of the matrix describes the emergence of new units as a result of fragmentation of larger units. For a given partition  $\kappa$  and given size of the newborn unit *i*, the rate of production of new units is equal to the product of the fragmentation rate  $(jb'_j)$ , the probability to fragment according to the given partition  $(q_{j,\kappa})$ , and the number of units of given size produced in the act of fragmentation with this partition  $(\pi_i(\kappa))$ . The value of an element  $a_{i,j}$  in the upper left triangle is equal to the sum of rates provided by all partitions available to clusters of size j,

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$$a_{i,j} = jb'_j \sum_{\kappa} q_{j,\kappa} \pi_i(\kappa).$$
(4)

The main diagonal  $a_{j,j}$  describes the changes in units numbers due to cell division and 44 fragmentation as well as the death of units. The first component of  $a_{j,j}$  captures that once a 45 unit of size i increase in size or fragments, the number of units of that size decreases. The 46 rates of decrease are equal to  $jb_jq_{j,(j+1)}$  due to cell division and  $jb'_j\sum_{\kappa}q_{j,\kappa}$  due to fragmen-47 tation. The second component is provided by a fragmentation with partition  $\kappa = j + 1$ , which 48 produce units of size equal to the size of parent. This leads to an increase in the number of 49 units of size j at rate  $jb'_{j}q_{j,j+1}\pi_{j}(j+1)$ , where  $\pi_{1}(1+1) = 2$  and  $\pi_{j}(j+1) = 1$  if j > 1. 50 The last component of  $a_{i,i}$  comes from the death of units, which leads to a decrease in their 51 number at rate  $d_j q_{j,(j+1)} + d'_j \sum_{\kappa} q_{j,\kappa}$ , where the first term describes the death rate in the ab-52 sence of the fragmentation and the second term describes the death rate of fragmenting units. 53

54 Combined, the diagonal elements of projection matrix are

$$a_{j,j} = -jb_j q_{j,(j+1)} - jb'_j \sum_{\kappa} q_{j,\kappa} + jb'_j q_{j,j+1} \pi_j (j+1) - d_j q_{j,(j+1)} - d'_j \sum_{\kappa} q_{j,\kappa}.$$
 (5)

<sup>56</sup> All elements of the projection matrix given by Eq. (3)-(5) are linear with respect to any <sup>57</sup> probability  $q_{j,\kappa}$ . As shown in [2], in this case the optimal life cycle is always deterministic, <sup>58</sup> independent of the parameter values, such as the division and death rates and the scenario of <sup>59</sup> the fragmentation cost.

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