Supplementary Material for "Emergent multicellular life cycles in filamentous bacteria due to density dependent population dynamics"

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S1 Algorithm scheme

Figure S1 illustrates schematically the algorithm used to simulate the dynamics of bacterial populations. The five steps are performed every iteration. In the first step, the population size is computed as the total number of cells, N_c. This quantity is used to compute the birth and death rates β and δ, that are density dependent. Secondly, a loop over all the filaments in the population begins. For each filament, the number of cell divisions and cell lyses are calculated and subsequently applied to the filament, that can

elongate (step 3) and break (step 4). The resulting new individuals are stored as filaments of the next iteration (step 5).

S2 Nonlinear birth and death rates

We tested the model with two different types of nonlinear birth and death rate functions. We used sigmoidal-shaped curves given by

$$\begin{aligned} \beta &= \frac{k_b}{k_b + N_c}, \quad k_b = \frac{\theta\, N_c^*}{1-\theta} \\ \delta &= \frac{N_c}{N_c + k_d}, \quad k_d = \frac{(1-\theta)\, N_c^*}{\theta} \end{aligned} \tag{1}$$

and hyperbolic functions of the form:

$$\begin{aligned} \beta &= \frac{1}{1 + e^{-a_1(N_c - c_1)}} \quad a_1 = -\frac{log(-(1-\theta)/\theta)}{N_c^* - c_1} \\ \delta &= \frac{1}{1 + e^{a_2(N_c - c_2)}} \quad a_2 = \frac{log(-(1-\theta)/\theta)}{N_c^* - c_2} \end{aligned} \tag{2}$$

where N_c is the total number of cells, N_c^* is the carrying capacity, θ is the turnover rate and $c_1, c_2 \in \mathbb{R}^+$. As for the linear case, the birth and rate functions in (1) and (2) satisfy $\beta(N_c^*) = \delta(N_c^*) = \theta$. The pie charts in Figure S2 illustrate the distribution of filament lengths when reaching carrying capacity obtained with β and δ as in (1) and (2). The plot shows that in both cases, the fraction of long filaments in the population (i.e. with more than 2 cells) increases as the turnover decreases. However, with sigmoidal functions, the trend is not very marked. On the other hand, the charts obtained with hyperbolic functions are qualitatively comparable with the ones of Figure 1d of the main text. This difference is due to the fact that the sigmoidal birth rate drops quickly towards the turnover value and does not allow a remarkable elongation of the filaments. The hyperbolic birth rate function instead maintains high values for a longer time, before

starting to decrease.

S3 Length distribution during the transient phase

Figure S4 show the mean length of the filaments calculated every iteration for two more values of θ in addition to $\theta = 0.9, 0.1$ presented in the main text. In Figure S4, for the case of turnover $\theta = 0.01$ the mean filament length does not exceed 1000 cells. For a turnover one order of magnitude lower ($\theta = 0.001$), the peak of the average length of filaments (up to 2000 cells) is significantly higher. Statistical support is given in table S2.

S4 Comparison of the theoretical and experimental distributions

Fig. S6 shows the distribution of filament lengths obtained from experimental (*Fibrella aestuarina*) and simulation data at different time points. The histograms indicate the percentage of filaments in a given class of length, in terms of number of cells. We used an approximation of 6.7 μm of the cell size as we have indicated in § 2.3 of the main text. There is a 1-to-1 correspondence between number of cells and bins. Hence, the first bin of the histograms indicates the percentage of single celled filaments, the second indicates the percentage of filaments with two cells, and so on. In order to make an illustrative comparison between the two datasets, we synchronize the two time-series according to the respective time or iteration at which they reach the carrying capacity. According to the OD curve, *F. aestuarina* reaches its carrying capacity after around 45 hours. For the theoretical data, we simulate the population dynamics for $\theta = 0.1$, using a starting conditions that that is comparable to the distribution of the experimental inoculum. With this initial condition, the population reaches the carrying capacity after 9

iterations. We have then

$$45 \text{ h} \simeq 9 \text{ iterations} \Rightarrow 5 \text{ h} \simeq 1 \text{ iteration}\,.$$

We considered the bell-shaped curve of the mean filament length vs time (Figure 2b in the main text) as a reference to choose the following five time points for comparison: the starting condition, one point at the left of the peak, the peak of the average length, one point at the right of the peak and the carrying capacity. The simulation-based histograms in Figure S6 show a qualitative match to trends in experimental data. A precise quantitative comparison is not possible, as we do not have an estimation of the turnover of the *F. aestuarina* strain against time. In the beginning, each population is mainly made up of short filaments. As the mean length reaches its peak, the population has filaments of various lengths. After the peak, the distribution of lengths is again shifted to the left, whereby short filaments are more abundant than the long ones.

S5 Mean length at carrying capacity and at the end of the experiment

Table S1 provides the mean filament length measurements when the cultures reach the carrying capacity and at the end of the experiment. The number of cells was calculated according to the same conversion used in the main text (see § 2.3 of the main text). Heterotrophic bacteria have a fast turnover, hence according to the model prediction (see Figure 1c in the main text), their mean filament length should be already close the one of the stationary state (two cells) when reaching carrying capacity. Data in Table S1 support this hypothesis: the average number of cells per filament of all heterotrophic species is near two when reaching carrying capacity. Cyanobacteria exhibit a much slower

generation time and hence a lower turnover. When reaching carrying capacity the filament length distribution is still far away from the stationary distribution of two cells per filament. Table 1 confirms this prediction, showing that at that point cyanobacteria are still very long.

The experiments performed in this study were not run in a chemostat. Therefore, after the culture reached carrying capacity, nutrient availability was decreasing and consequently death rate was increasing. The breakage process has been accelerated and the carrying capacity of the population gradually dropped below the initial one. This observation explains why at the end of the heterotroph experiments, the average filament length is below two.

S6 Statistical tests

For the simulation data, significance of the increase and decrease of mean filament length at different time points was proved by comparing the distribution of the mean at three reference points, namely the starting condition, the peak of the filament length and the time at which the population reaches its carrying capacity. Since the data were not normally distributed, we used a Wilcoxon rank sum test as a nonparametric hypothesis test. For each tested pair and for every turnover rate, the null hypothesis that the two compared samples come from distributions with equal medians was rejected, as shown in table S2. The rank sum test was performed with MATLAB statistics toolbox (www.mathworks.ch/products/statistics/).

For the experimental data, significance of the increase and decrease of filament length at different time points was proved by a one-way analysis of variance (ANOVA, significance level of 0.05) followed by a Tukey's test as a multiple comparison procedure. For each bacterial species, data at different time points were considered as independent samples

containing mutually independent observations. In all cases, in order to match the requirement of normality of the distribution, we transformed the sampled data by taking their natural logarithm. The ANOVA test compares the sample means and returns the p-value under the null hypothesis that all samples are drawn from populations with the same mean. However, ANOVA evaluates the hypothesis that the samples all have the same mean against the alternative that the means are not all the same. In order to determine which pairs of means were significantly different, we performed a multiple comparison using the Tukey's honestly significant difference criterion. The output of the latter test for each species is shown in tables S3, S4, S5, S6, S7. In the tables, for each time point pair we show the estimated difference in means and a confidence interval for this difference. If the confidence interval does not contain 0.0, the samples means are significantly different at the 0.05 level. If the confidence interval contains 0.0, than the the samples means are not significantly different at the 0.05 level. Bolded intervals correspond to the comparison between the inoculum and peak and between peak and carrying capacity. These three points were taken as a reference to prove significant increase/decrease of mean length. Both ANOVA and multiple comparison have been performed with MATLAB statistics toolbox. According to the ANOVA test, the hypothesis that the means are all the same was rejected in the case of all species ($p < 0.05$).

Statistical support for different distributions of filament length when reaching carrying capacity is shown in Tables S8 and S9, for the simulation and the experimental data respectively. In the case of the simulations, we compared the distribution for different turnovers at that time point. The datasets of the means of 1000 runs were normally distributed. Hence we applied a one-way ANOVA followed by a multiple comparison using the Tukey's honestly significant difference criterion. In the case of experiments, we compared the distribution of different species when the population size reached its

carrying capacity. We took the same approach of a one-way ANOVA coupled with a multiple comparison, after a logarithmic transformation of the data to match the assumption of normality.

S7 Serial Transfer experiment and simulation

Simulation. We run a series of successive simulations, each one consisting of 20 iterations (Fig. 5a in the main text). The initial curve was obtained with the default starting condition of one cell. When the average filament length of the initial culture was at its maximum, a simulation of a new culture was started. The new simulation was initialized with one filament of the length corresponding to the average length at the peak of the previous culture (averaged over 50 runs). The same steps were repeated for each newly started culture. Each new simulation with low population density emulates a transfer to a fresh medium. The choice of a carrying capacity higher than the default of 5000 cells would have allowed the setting of a distribution of filaments instead of a single filament as a starting condition. However, increasing the carrying capacity leads to a considerably longer computational time. Thereby we opted for an approximation using the mean filament length as starting condition for each successive transfer.

Laboratory experiment. Bacteria were cultivated the same way as in the batch culture experiments. After 17 hours the first transfer was done, whereby five mL of the growing culture were transferred into 50-mL flasks containing 20 mL of R_2A medium. The initial culture was incubated on a shaker (120 rpm) at 29 ℃ for 5 hours, and then transferred again. Subsequently the new transfers were done with 3 hours interval. Before each transfer, sample aliquots were fixed with formaldehyde (final concentration, 2%) and used for microscopic length observation. Pictures were taken with a digital camera (Color View, Soft Imaging System) connected to a light microscope (Olympus BX 51, Germany)

using a 4x objective. At least 450 filaments were counted per time point.

S8 Estimation of the time of first spilt

The assumptions of the model presented in the main text allow the derivation of the estimated iteration at which the mean filament length in the population starts the decreasing phase. Recalling the definition of the birth and death rate functions β and δ as $\beta(N_c) = -c_1 N_c + 1,\ c_1 = (1-\theta)/N_c^*$ and $\delta(N_c) = c_2 N_c,\ c_2 = \theta/N_c^*$, and setting $N_c = i$, the probability that the next event is a death is given by

$$\text{Prob(death)} = \frac{\delta}{\beta+\delta} = \frac{(\theta i)/N_c^*}{1-[(1-\theta)i]/N_c^* + (\theta i)/N_c^*} \sim \frac{\theta i}{N_c^*}$$

where the last approximation holds if $i \ll N_c^*$. The probability that an event is a birth is hence $1 - \frac{\theta i}{N_c^*}$. Assuming one single cell as a starting condition, the probability that the first m events are births is given by

$$\prod_{i=1}^{m} \left(1 - \frac{\theta i}{N_c^*}\right) \sim e^{-\sum_{i=1}^{m} \frac{\theta i}{N_c}} = e^{-\frac{\theta\, m(m+1)}{2N_c}} \sim e^{-\frac{\theta\, m^2}{2N_c}}\,, \tag{3}$$

where for the first approximation we used the fact that for any $\varepsilon \ll 1$,

$$1 - \varepsilon = \exp(\log(1-\varepsilon)) = \exp(-\varepsilon - \frac{1}{2}\varepsilon - \frac{1}{3}\varepsilon \dots) \sim \exp(-\varepsilon)\,.$$

One can then use eq. (3) to estimate the number of cells occurring before the first filament split. For example one can start by assigning the typical value of $1/e$ to the probability defined by (3). We have then

$$e^{-\frac{\theta\, m^2}{2N_c}} = 1/e \Leftrightarrow \frac{\theta\, m^2}{2N_c} = 1 \Leftrightarrow m = \sqrt{(2N_c^*)/\theta}\,.$$

If we suppose that at any of the first m events every cell divides, and considering that the initial filament is a single cell, we expect to have 2^t cells after t iterations and hence

$$2^t \approx m \Rightarrow t \approx \log_2 m\,. \tag{4}$$

In (4), t represents the approximate iteration of first filament breakage. The values t obtained by plugging in the values of N_c^* and θ used in the paper fit well with the results showed in Figure 2 of the main text and Figure S3. The time of first split coincides roughly with the iteration at which the average length of filaments reaches its peak. For $\theta = 0.9, 0.1, 0.01, 0.001$ we have $t = 6.7, 8.2, 10, 11.5$, observed in Figures 2 of the main text and S3 respectively. The case of a different initial condition, where there is more than one single cell, can be treated similarly and has been tested. By letting the product in (3) to start from a value $N_0 > 1$, we obtain $m_0 = \sqrt{(2N_c^*/N_0)/\theta}$. The initial condition used to produce Figure S5 has been chosen to test the validity of the latter formula for m_0. The obtained result fitted again the predicted iteration of first split given by $t_0 \approx \log_2 m_0 = 4.6$, as shown in Figure S7.

S9 Stationary distribution of filament length based on an analogous continuous time model

By considering the possible events (birth or death of a cell) in any time interval, one can define the following model for the evolution of the filamentation process in continuous time. Let $N_j(t)$, $j \geq 1$, denote the number of filaments of length j in the system at time t. Then the Markovian transition rates out of the state $\overrightarrow{N} := (N_1, N_2, \ldots)$ are given by

$$\overrightarrow{N} \;\to\; \overrightarrow{N} + \hat{\mathbf{e}}^{(j+1)} - \hat{\mathbf{e}}^{(j)} \qquad \text{at rate} \quad j\, b(\overrightarrow{N})\, N_j, \quad j \geq 1 \tag{5}$$

$$\overrightarrow{N} \;\to\; \overrightarrow{N} + 2\hat{\mathbf{e}}^{(j)} - \hat{\mathbf{e}}^{(2j+1)} \qquad \text{at rate} \quad d(\overrightarrow{N})\, N_{2j+1}, \quad j \geq 1 \tag{6}$$

$$\overrightarrow{N} \;\to\; \overrightarrow{N} + \hat{\mathbf{e}}^{(j-k-1)} + \hat{\mathbf{e}}^{(k)} - \hat{\mathbf{e}}^{(j)} \qquad \text{at rate} \quad 2\, d(\overrightarrow{N})\, N_j, \quad 0 \leq k < \frac{j-1}{2},\ j \geq 1 \tag{7}$$

where $\hat{\mathbf{e}}^{(j)}, j \geq 1$, denotes the j-th unit vector, and $b(\overrightarrow{N})$, $d(\overrightarrow{N})$ represent the *per capita* birth and death rates respectively. The latter are given by

$$b(\overrightarrow{N}) \;:=\; b - c_1 N_c/N_c^*, \qquad d(\overrightarrow{N}) \;:=\; c_2 N_c/N_c^*,$$

where $b = c_1 + c_2$, $N_c := \sum_{j\geq 1} jN_j$ is the total number of cells in the system, and N_c^* is the value of N_c at the carrying capacity. In equations (5)-(7), the first transition refers to cell birth in a filament of length j, whereby filaments of length j lose one unit ($-\hat{\mathbf{e}}^{(j)}$) and those of length $j+1$ increase by one ($+\hat{\mathbf{e}}^{(j+1)}$). The second transition refers to cell death at the center of a filament with an odd number of cells. In this case, a filament with $2j+1$ cells breaks ($-\hat{\mathbf{e}}^{(2j+1)}$) in two filaments of length j ($+2\hat{\mathbf{e}}^{(j)}$). The third transition represents the case of a cell death at any position of a filament other than the exact center, whereby a filament of length j breaks at position $k+1$ ($-\hat{\mathbf{e}}^{(j)}$) producing a filament of length $j-k-1$ ($+\hat{\mathbf{e}}^{(j-k-1)}$) and one of length k ($+\hat{\mathbf{e}}^{(k)}$).

In the long term, when there are many cells in the system, the ratios $n_j := N_j/N_c^*$ can be thought of as more or less continuous quantities, with behavior the average of what is predicted by the transition rates in (5)-(6). This yields the following differential equations describing the evolution of the n_j:

$$\frac{dn_j}{dt} \;=\; (b - c_1 m)(j-1)n_{j-1} - j(b - (c_1 - c_2)m)n_j + 2c_2 m \sum_{i>j} n_i, \tag{8}$$

where $m := \sum_{j\geq 1} jn_j$ represents the total number of cells as a proportion of the carrying capacity. Formally adding over $j \geq 1$, one obtains

$$\frac{dx}{dt} \;=\; c_2 m(m-2x), \tag{9}$$

where $x := \sum_{j\geq 1} n_j$ is the total number of filaments weighted by the carrying capacity. Then, recalling $c_1 + c_2 = b$,

$$\frac{dm}{dt} \;=\; b(1-m)m. \tag{10}$$

Equation (10) is the well-known logistic equation, and can be integrated to show exponentially fast convergence of $m(t)$ to its limit 1; it then follows by integrating (9) that $x(t) \to 1/2$. Considering that the average length of filaments $\overline{L}$ can be derived as

$$\overline{L} = \frac{m}{x} = \frac{\sum_{j\geq 1} jN_j/N_c^*}{\sum_{j\geq 1} N_j/N_c^*} = \frac{\sum_{j\geq 1} jN_j}{\sum_{j\geq 1} N_j}$$

and that, as mentioned above, $m(t) \to 1, x(t) \to 1/2$, we have that

$$\overline{L} \to \frac{1}{1/2} = 2.$$

In fact, more is true: the equations (8) have a stationary solution with $m = 1$ and $n_j = 2^{-j}$, $j \geq 1$, so that the equilibrium distribution of filament lengths is geometric with mean 1/2.

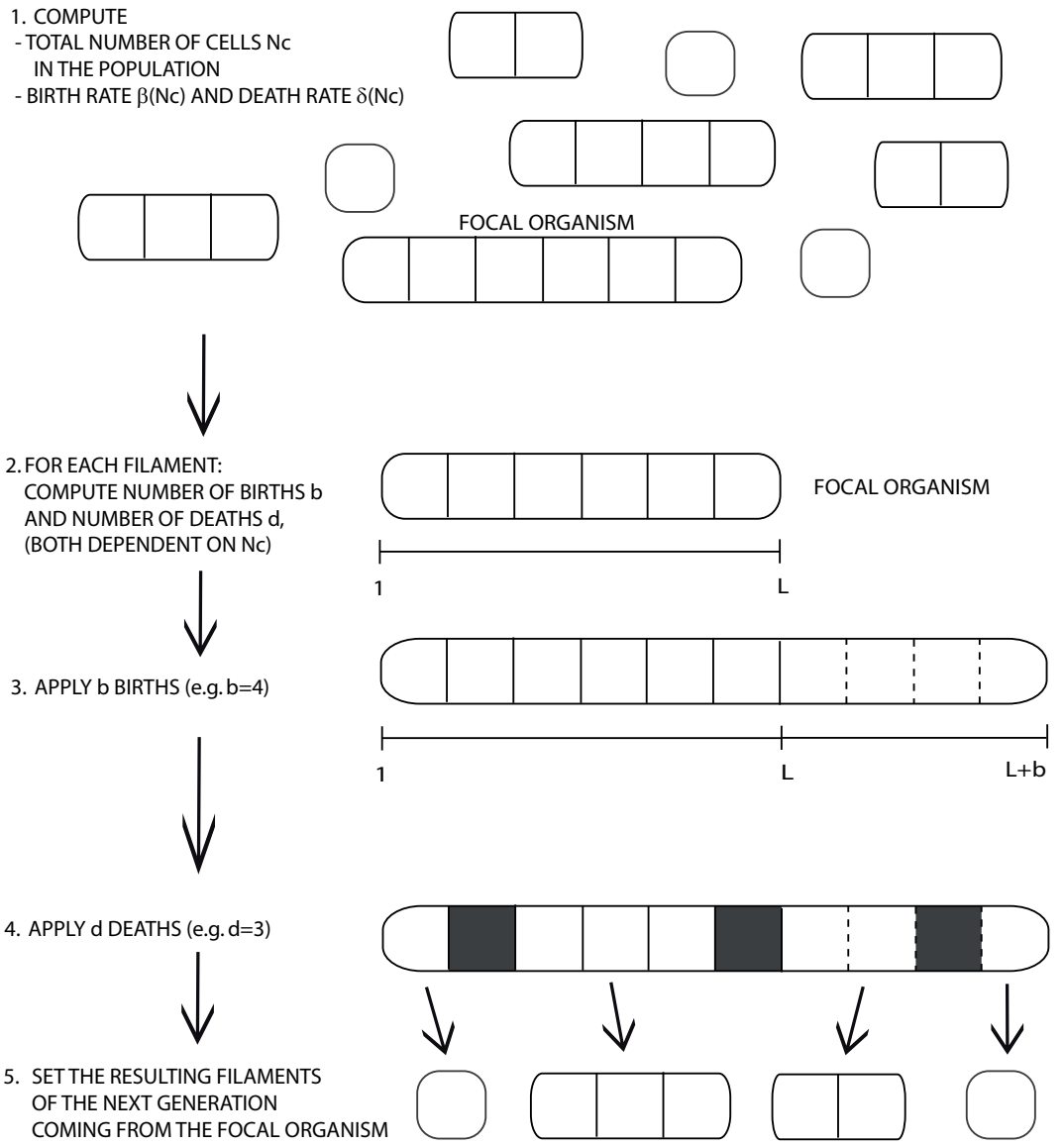

Figure S 1: Schematic view of the algorithm describing how filament length distributions are affected by processes governing birth and death rates of cells.

	Carrying capacity		Last datapoint	
Species	Mean length	Confidence interval	Mean length	Confidence interval
R. lutea A	3.1	[0.7 , 9.1]	1.5	[0.7 , 3.9]
R. lutea B	4.3	[0.9 , 13]	1.8	[0.6 , 5]
F. limi	2.7	[0.7 , 10.4]	1.4	[0.4 , 4.1]
F. aestuarina A	4.2	[0.6 , 18.8]	1	[0.3 , 2.8]
F. aestuarina B	3.8	[0.7 , 15.9]	1.2	[0.3 , 4.4]
N. muscorum A	87.9	[9 , 305.1]	74.7	[5.7 , 274.7]
N. muscorum B	102	[10.2 , 324.6]	74.4	[7.8 , 243.8]
A. variabilis A	166.3	[11.3 , 378.3]	30.7	[3.7 , 119.4]
A. variabilis B	160.3	[28.1 , 370]	25.3	[4 , 92.3]

Table S 1: Mean length of filaments expressed in number of cells when reaching carrying capacity and at the end of the experiment. The confidence interval is derived from the 25th and 75th percentiles of the measured lengths. Capital letters next to the species name indicate the experiment.

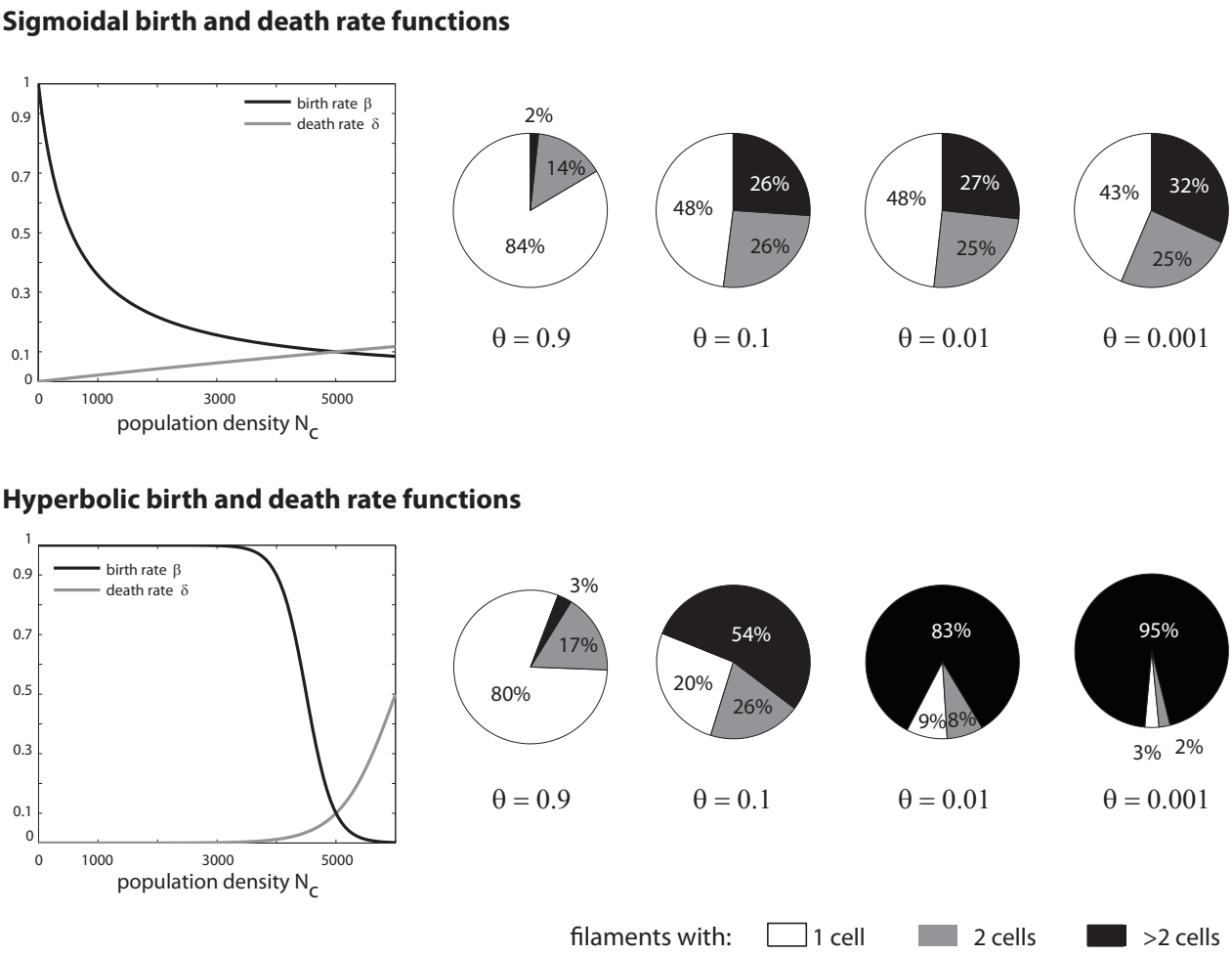

Figure S 2: Distribution of filament length when reaching carrying capacity at $\theta = 0.1$, for the case of nonlinear birth and death rates.

Turnover	Pair compared	p-value	Significant difference
$\theta = 0.9$	Starting point - Peak	0	yes
	Peak - carrying capacity	0	yes
$\theta = 0.1$	Starting point - Peak	0	yes
	Peak - carrying capacity	0	yes
$\theta = 0.01$	Starting point - Peak	0	yes
	Peak - carrying capacity	0	yes
$\theta = 0.001$	Starting point - Peak	0	yes
	Peak - carrying capacity	0	yes

Table S 2: Wilcoxon rank-sum test to prove significant increase and decrease in mean filament length in the simulation data, for different turnovers.

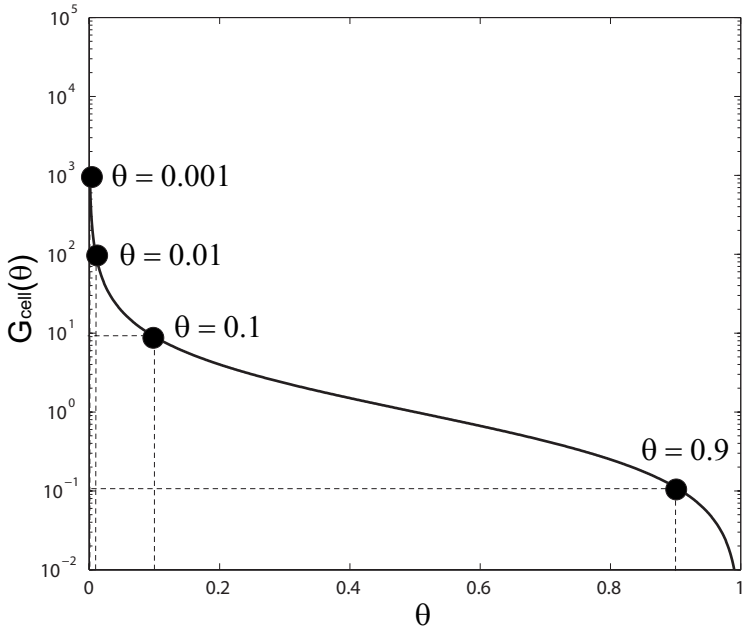

Figure S 3: Plot of the function of generation time$G_{cell}(\theta) = \theta \mapsto (1-\theta)/\theta$ for $\theta \in [0,1]$ (log scale). The generation time of a cell is a decreasing function of the turnover rate. The dots indicate the generation time $G_{cell}(\theta)$ at carrying capacity correspondent to the values of θ used in the simulations.

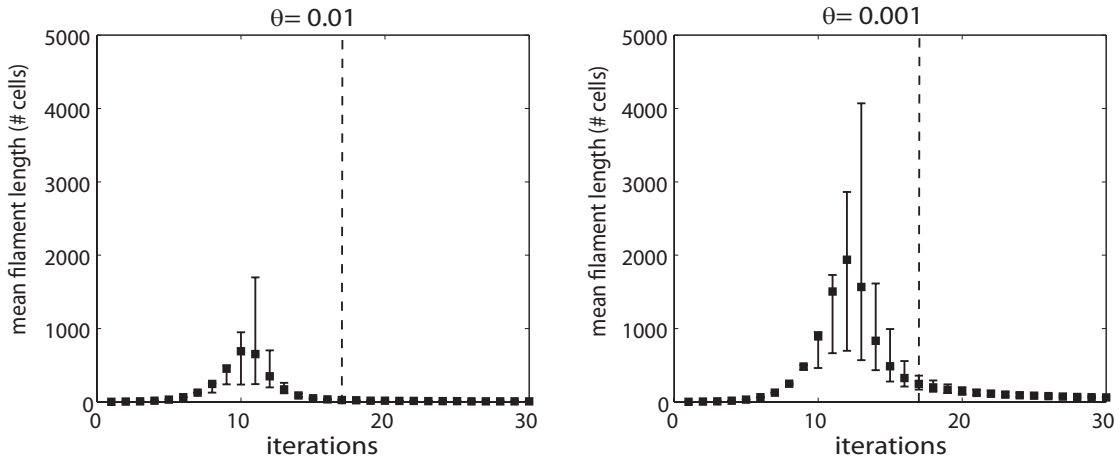

Figure S 4: The mean filament length for 30 iterations has been tracked for $\theta = 0.01$ and $\theta = 0.001$ and averaged over 1000 runs. Edges of the error bars correspond to the 2.5th and 97.5th percentiles of the distribution of the mean filament lengths in the 1000 runs. As already shown in the main text, in the transient phase filaments are shorter if the turnover is high (left) while they can be considerably longer for low turnovers (right). The dotted line indicates the iteration at which the carrying capacity is reached.

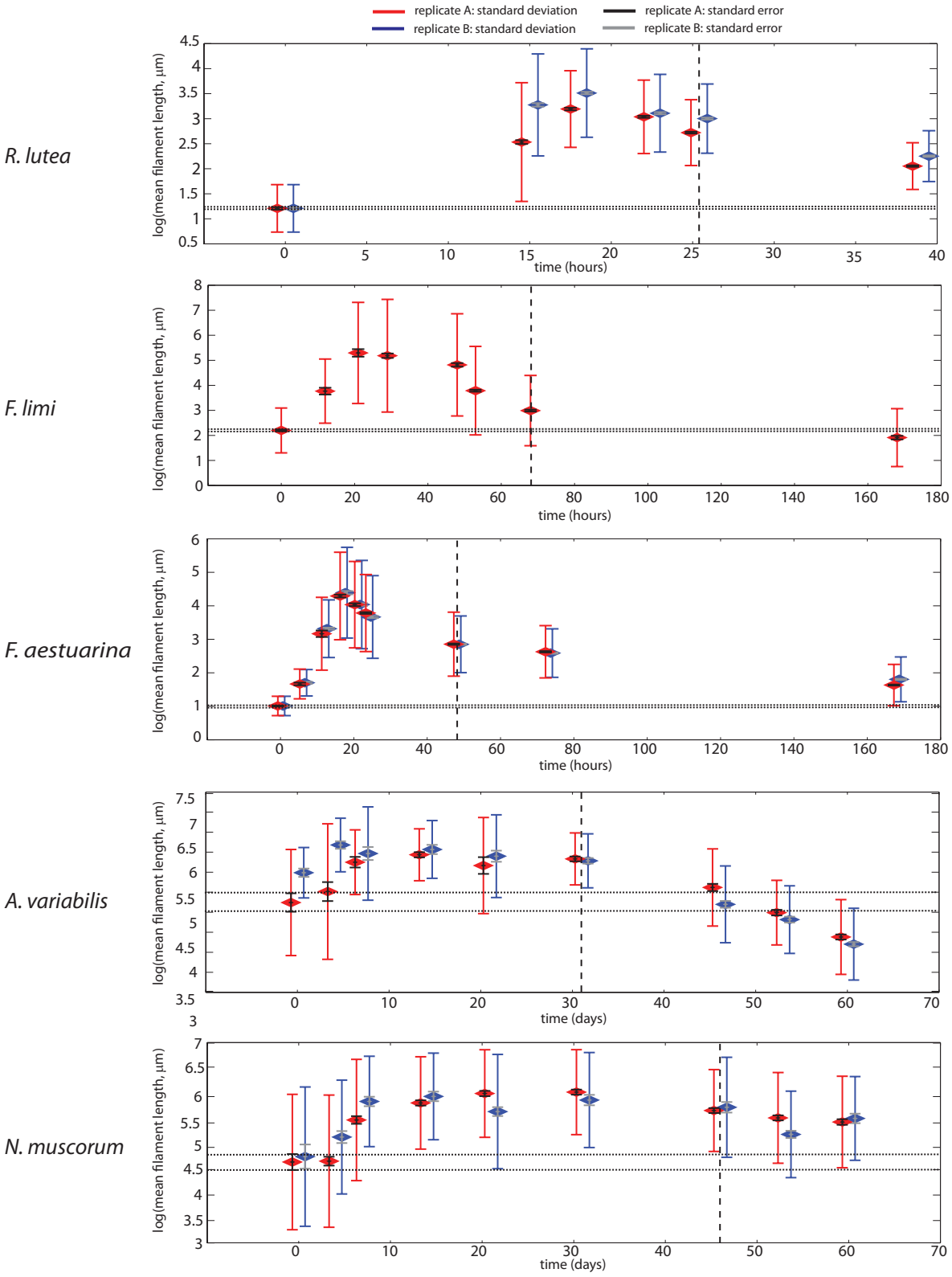

Figure S 5: Empirical measurements showing mean length of bacteria against time, after logarithmic transformation of the data. Standard deviation of the observation and standard error of the mean are shown. Diamonds indicate the logarithm of the mean length at each time point. The zero time point corresponds to the inoculum. The dotted vertical line indicates the time at which the carrying capacity was reached. The horizontal dotted lines indicate the interval determined by the standard error of the inoculum. It helps the reader in identifying the time points at which the mean length falls in the same range. The lines are indicated only for replicate A.

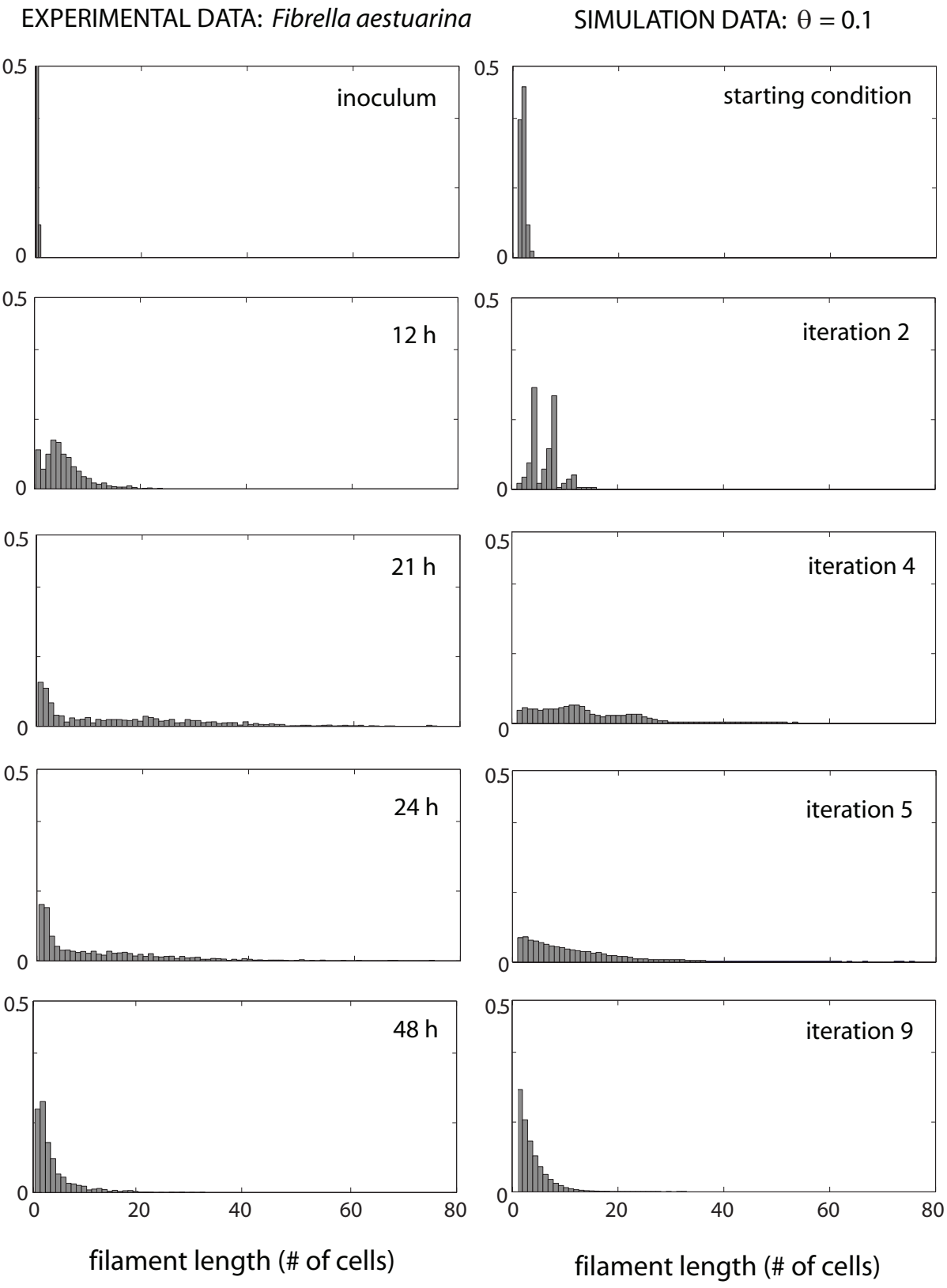

Figure S 6: Histograms of the distribution of filament lengths according to experimental data (left) and simulations (right).

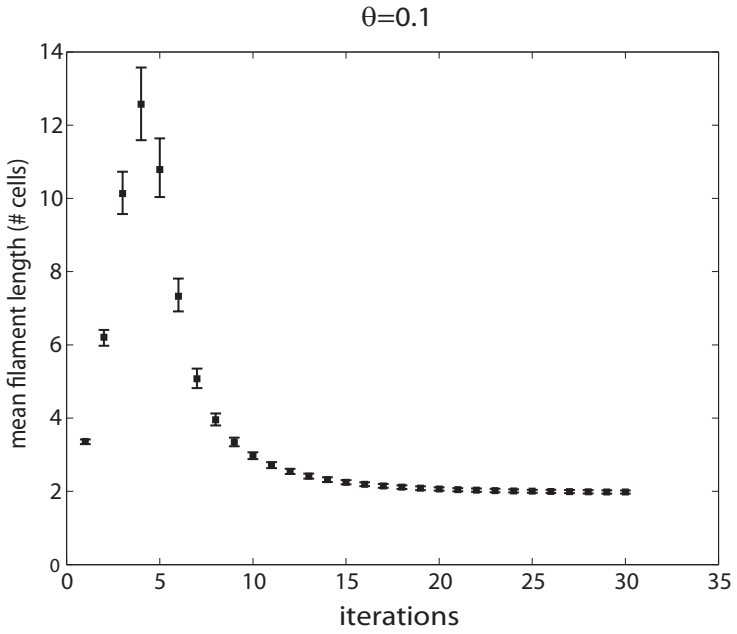

Figure S 7: Mean filament length over 1000 runs when the starting condition for the simulation is comparable to the distribution of the experimental inoculum of *Fibrella aestuarina*. Edges of the error bars correspond to the 2.5th and 97.5th percentiles of the computed means.

Time 1	Time 2	estimated difference in means	95% confidence interval of the difference	Significant difference
1	2	-1.3245	[-1.4587 -1.1903]	yes
1	3	**-1.9843**	**[-2.1198 -1.8488]**	**yes**
1	4	-1.8289	[-1.9572 -1.7007]	yes
1	5	-1.5131	[-1.6408 -1.3854]	yes
1	6	-0.8446	[-0.9781 -0.7111]	yes
2	3	-0.6598	[-0.7624 -0.5572]	yes
2	4	-0.5044	[-0.5973 -0.4116]	yes
2	5	-0.1886	[-0.2807 -0.0965]	yes
2	6	0.4799	[0.3799 0.5799]	yes
3	4	0.1554	[0.0607 0.2500]	yes
3	5	**0.4712**	**[0.3773 0.5651]**	**yes**
3	6	1.1397	[1.0380 1.2414]	yes
4	5	0.3158	[0.2327 0.3990]	yes
4	6	0.9843	[0.8925 1.0762]	yes
5	6	0.6685	[0.5774 0.7596]	yes

Table S 3: Multiple comparison for *R. lutea*. The numbers in bold pertain to comparisons between the time points taken as a reference to prove the increase or decrease of filament length (between inoculum, peak and carrying capacity). Time points 1, 3 and 5 correspond to the inoculum, peak and carrying capacity, respectively.

Time 1	Time 2	estimated difference in means	95% confidence interval of the difference	Significant difference
1	2	-0.7856	[-1.0727 -0.4984]	yes
1	**3**	**-1.5483**	[**-1.7629 -1.3337**]	**yes**
1	4	-1.4924	[-1.6317 -1.3531]	yes
1	5	-1.3098	[-1.4425 -1.1772]	yes
1	6	-0.7944	[-0.9058 -0.6830]	yes
1	7	-0.3966	[-0.5153 -0.2779]	yes
1	8	0.1428	[-0.0432 0.3288]	no
2	3	-0.7627	[-1.0944 -0.4311]	yes
2	4	-0.7068	[-0.9955 -0.4181]	yes
2	5	-0.5243	[-0.8098 -0.2387]	yes
2	6	-0.0088	[-0.2851 0.2675]	no
2	7	0.3889	[0.1096 0.6683]	yes
2	8	0.9284	[0.6145 1.2423]	yes
3	4	0.0559	[-0.1608 0.2726]	no
3	5	0.2385	[0.0260 0.4509]	yes
3	6	0.7539	[0.5540 0.9538]	yes
3	**7**	**1.1517**	[**0.9476 1.3557**]	**yes**
3	8	1.6911	[1.4418 1.9404]	yes
4	5	0.1826	[0.0465 0.3186]	yes
4	6	0.6980	[0.5826 0.8134]	yes
4	7	1.0958	[0.9733 1.2183]	yes
4	8	1.6352	[1.4468 1.8236]	yes
5	6	0.5154	[0.4082 0.6227]	yes
5	7	0.9132	[0.7984 1.0280]	yes
5	8	1.4526	[1.2691 1.6362]	yes
6	7	0.3978	[0.3084 0.4871]	yes
6	8	0.9372	[0.7684 1.1060]	yes
7	8	0.5394	[0.3657 0.7131]	yes

Table S 4: Multiple comparison for *F. limi*. Time points 1,3 and 7 correspond to the inoculum, peak and carrying capacity respectively.

Time 1	Time 2	estimated difference in means	95% confidence interval of the difference	Significant difference
1	2	-0.6569	[-0.9532 -0.3606]	yes
1	3	-2.1569	[-2.3096 -2.0042]	yes
1	4	**-3.2831**	**[-3.4351 -3.1311]**	**yes**
1	5	-3.0246	[-3.1738 -2.8753]	yes
1	6	-2.7745	[-2.9046 -2.6443]	yes
1	7	-1.8450	[-1.9741 -1.7159]	yes
1	8	-1.6181	[-1.7553 -1.4810]	yes
1	9	-0.6248	[-0.7617 -0.4879]	yes
2	3	-1.5000	[-1.7937 -1.2063]	yes
2	4	-2.6262	[-2.9195 -2.3329]	yes
2	5	-2.3677	[-2.6595 -2.0758]	yes
2	6	-2.1176	[-2.4002 -1.8350]	yes
2	7	-1.1881	[-1.4702 -0.9060]	yes
2	8	-0.9612	[-1.2471 -0.6753]	yes
2	9	0.0321	[-0.2537 0.3179]	no
3	4	-1.1262	[-1.2730 -0.9795]	yes
3	5	-0.8677	[-1.0116 -0.7238]	yes
3	6	-0.6176	[-0.7416 -0.4936]	yes
3	7	0.3119	[0.1890 0.4348]	yes
3	8	0.5388	[0.4074 0.6701]	yes
3	9	1.5321	[1.4010 1.6632]	yes
4	5	0.2585	[0.1154 0.4017]	yes
4	6	0.5086	[0.3856 0.6317]	yes
4	7	**1.4381**	**[1.3161 1.5601]**	**yes**
4	8	1.6650	[1.5345 1.7955]	yes
4	9	2.6583	[2.5281 2.7885]	yes
5	6	0.2501	[0.1304 0.3698]	yes
5	7	1.1796	[1.0610 1.2981]	yes
5	8	1.4064	[1.2792 1.5337]	yes
5	9	2.3998	[2.2727 2.5268]	yes
6	7	0.9295	[0.8361 1.0228]	yes
6	8	1.1563	[1.0521 1.2606]	yes
6	9	2.1497	[2.0458 2.2536]	yes
7	8	0.2269	[0.1240 0.3298]	yes
7	9	1.2202	[1.1176 1.3228]	yes
8	9	0.9933	[0.8808 1.1059]	yes

Table S 5: Multiple comparison for *F. aestuarina*. Time points 1, 4 and 7 correspond to the inoculum, peak and carrying capacity respectively.

Time 1	Time 2	estimated difference in means	95% confidence interval of the difference	Significant difference
1	2	-0.2734	[-0.9283 0.3815]	no
1	3	-1.0062	[-1.7081 -0.3043]	yes
1	4	**-1.1920**	**[-1.7798 -0.6042]**	**yes**
1	5	-0.9229	[-1.6446 -0.2013]	yes
1	6	-1.0886	[-1.6670 -0.5103]	yes
1	7	-0.3759	[-0.9548 0.2030]	no
1	8	0.2530	[-0.3166 0.8227]	no
1	9	0.8612	[0.3136 1.4087]	yes
2	3	-0.7328	[-1.3658 -0.0997]	yes
2	4	-0.9185	[-1.4221 -0.4150]	yes
2	5	-0.6495	[-1.3044 0.0054]	no
2	6	-0.8152	[-1.3077 -0.3227]	yes
2	7	-0.1025	[-0.5956 0.3907]	no
2	8	0.5265	[0.0441 1.0088]	yes
2	9	1.1346	[0.6786 1.5906]	yes
3	4	-0.1858	[-0.7491 0.3775]	no
3	5	0.0832	[-0.6187 0.7851]	no
3	6	-0.0824	[-0.6359 0.4710]	no
3	7	0.6303	[0.0762 1.1844]	yes
3	8	1.2592	[0.7148 1.8036]	yes
3	9	1.8673	[1.3461 2.3886]	yes
4	5	0.2690	[-0.3188 0.8568]	no
4	6	**0.1033**	**[-0.2956 0.5023]**	**no**
4	7	0.8161	[0.4163 1.2158]	yes
4	8	1.4450	[1.0587 1.8313]	yes
4	9	2.0531	[1.7003 2.4060]	yes
5	6	-0.1657	[-0.7440 0.4127]	no
5	7	0.5470	[-0.0319 1.1260]	no
5	8	1.1760	[0.6063 1.7457]	yes
5	9	1.7841	[1.2365 2.3317]	yes
6	7	0.7127	[0.3270 1.0985]	yes
6	8	1.3417	[0.9699 1.7134]	yes
6	9	1.9498	[1.6129 2.2867]	yes
7	8	0.6289	[0.2563 1.0016]	yes
7	9	1.2371	[0.8992 1.5749]	yes
8	9	0.6081	[0.2863 0.9299]	yes

Table S 6: Multiple comparison for *A. variabilis*. Time points 1,4 and 6 correspond to the inoculum, peak and carrying capacity respectively.

Time 1	Time 2	estimated difference in means	95% confidence interval of the difference	Significant difference
1	2	-0.0195	[-0.4886 0.4496]	no
1	3	-0.9441	[-1.4060 -0.4821]	yes
1	4	-1.3273	[-1.7791 -0.8754]	yes
1	5	-1.5394	[-1.9966 -1.0821]	yes
1	6	**-1.5702**	**[-2.0264 -1.1140]**	yes
1	7	-1.1567	[-1.6141 -0.6993]	yes
1	8	-0.9917	[-1.4422 -0.5413]	yes
1	9	-0.8992	[-1.3577 -0.4408]	yes
2	3	-0.9246	[-1.2437 -0.6055]	yes
2	4	-1.3078	[-1.6122 -1.0034]	yes
2	5	-1.5199	[-1.8322 -1.2076]	yes
2	6	-1.5507	[-1.8615 -1.2399]	yes
2	7	-1.1372	[-1.4497 -0.8247]	yes
2	8	-0.9723	[-1.2745 -0.6700]	yes
2	9	-0.8798	[-1.1938 -0.5657]	yes
3	4	-0.3832	[-0.6764 -0.0900]	yes
3	5	-0.5953	[-0.8967 -0.2940]	yes
3	6	-0.6262	[-0.9260 -0.3263]	yes
3	7	-0.2126	[-0.5142 0.0890]	no
3	8	-0.0477	[-0.3386 0.2432]	no
3	9	0.0448	[-0.2584 0.3480]	no
4	5	-0.2121	[-0.4978 0.0736]	no
4	6	-0.2430	[-0.5271 0.0412]	no
4	7	0.1706	[-0.1154 0.4566]	no
4	8	0.3355	[0.0608 0.6102]	yes
4	9	0.4280	[0.1403 0.7157]	yes
5	6	-0.0308	[-0.3234 0.2617]	no
5	7	0.3827	[0.0883 0.6771]	yes
5	8	0.5476	[0.2642 0.8311]	yes
5	9	0.6401	[0.3441 0.9362]	yes
6	7	**0.4135**	**[0.1207 0.7064]**	yes
6	8	0.5785	[0.2967 0.8603]	yes
6	9	0.6710	[0.3765 0.9654]	yes
7	8	0.1649	[-0.1188 0.4486]	no
7	9	0.2574	[-0.0389 0.5537]	no
8	9	0.0925	[-0.1929 0.3779]	no

Table S 7: Multiple comparison for *N. muscorum*. Time points 1,6 and 7 correspond to the inoculum, peak and carrying capacity respectively.

Turnover 1	Turnover 2	estimated difference in means	95% confidence interval of the difference	Significant difference
0.001	0.01	222.7728	[219.4576 226.0879]	yes
0.001	0.1	244.8196	[241.5044 248.1347]	yes
0.001	0.9	247.1738	[243.8587 250.4890]	yes
0.01	0.1	22.0468	[18.7316 25.3620]	yes
0.01	0.9	24.4011	[21.0859 27.7162]	yes
0.1	0.9	2.3542	[-0.9609 5.6694]	no

Table S 8: Multiple comparison for the distribution of filament lengths when reaching carrying capacity for different turnovers.

Species 1	Species 2	estimated difference in means	95% confidence interval of the difference	Significant difference
R. lutea	*F. limi*	0.2258	[0.1411 0.3104]	yes
R. lutea	*F. aestuarina*	-0.1325	[-0.2086 -0.0564]	yes
R. lutea	*N. muscorum*	-2.7501	[-2.8968 -2.6033]	yes
R. lutea	*A. variabilis*	-3.6092	[-3.8242 -3.3942]	yes
F. limi	*F. aestuarina*	-0.3583	[-0.4350 -0.2815]	yes
F. limi	*N. muscorum*	-2.9758	[-3.1230 -2.8287]	yes
F. limi	*A. variabilis*	-3.8350	[-4.0502 -3.6197]	yes
F. aestuarina	*N. muscorum*	-2.6176	[-2.7599 -2.4752]	yes
F. aestuarina	*N. muscorum*	-3.4767	[-3.6887 -3.2647]	yes
N. muscorum	*A. variabilis*	-0.8591	[-1.1055 -0.6128]	yes

Table S 9: Multiple comparison within species of the distribution of filament length when the population reaches its carrying capacity.