Cellular dynamics under time-varying conditions

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Building on the known scaling law that a single timescale, a cellular unit of time, governs stochastic growth and division of individual bacterial cells under constant growth conditions, here we articulate an analogous ansatz for time-varying growth conditions. We propose that a dynamic rescaling of the cellular unit of time captures the predominant effect of external variations in conditions. Using this temporal scaling ansatz, we derive exact analytic results for how the time-dependent cell age distribution adapts to changing conditions. Our results reveal the natural representation for these time-dependent dynamics. When recast in terms of the new representation, the cell age distribution evolves under time-invarant rules even as growth conditions remain dynamic! This result corresponds to the generalization of the scaling law for constant growth condition. Finally, we provide a prescription for convenient experimental tests of the temporal scaling ansatz.

Living organisms routinely experience dynamic environments and adjust their internal state accordingly. Yet, biophysical principles that govern their physiological adaptation to unpredictable temporal variations in external conditions remain to be uncovered [1, 2]. The challenge in experimentally addressing this question stems from the vast size of all possible responses, which cannot be systematically tabulated to search for patterns, even in the era of high-throughput high-precision experiments and AI-based analyses. This issue is exacerbated in the absence of a clear separation of timescales, such as between the timescale of extrinsic variation in ambient conditions and the typical lifetime of the organism [2]. Performing experiments representative of scenarios that span the range of possible environments a given organism may experience over time is impractical, as these environments are inherently high-dimensional. Even for experiments involving the simplest unicellular organisms, such as bacteria, the challenge remains [2–8]..

To break this impasse, here we take a theoretical route to substantial dimension reduction of the problem [9, 10]. We focus on growth and division dynamics of individual bacterial cells in time-varying growth conditions, first recapitulating known results for constant growth conditions [11–14]. High-precision single-cell measurements on large ensembles of statistically identical non-interacting bacterial cells have revealed that under constant growth conditions, a single timescale—an emergent cellular unit of time—governs stochastic growth and division dynamics [11–16]. While the numerical value of this timescale changes between growth conditions, the dynamics of growth and division of individual bacterial cells are universal across growth conditions in terms of rescaled dimensionless variables. The cellular timescale can be experimentally calibrated for a given (constant) growth condition using any one of the individual-cell-size growth rate, κ; the mean interdivision time, $\langle\tau\rangle$; or the population numbers growth rate, k [11–13, 15].

Under constant growth conditions, the mean-rescaled division-time distributions are universal across growth conditions [12, 13]. In other words, the different division time distributions corresponding to different (constant) growth conditions are simply rescaled versions of each other. This scaling law follows from the previously stated result that a single emergent timescale governs stochastic growth and division processes under time-invariant conditions.

Instead of focusing on individual cells, we could consider the population dynamics through an ensemble perspective that correctly accounts for the underlying stochasticity in division events [13, 17]. The population cell-age distribution, $n(t, \tau)$, which tracks the number density of cells of a given age τ (since the last division event), at a time t, serves as a convenient bridge between the single-cell and population perspectives. Under constant growth conditions, the interdivision time distribution and population cell age distribution are mathematically related, and uniquely determine each other [13]. The scaling law for mean-rescaled division time distributions thus implies an equivalent scaling law in the population perspective: the mean-rescaled cell age distributions from different (constant) growth conditions undergo a scaling collapse.

In this work, we propose that a dynamic rescaling of the cellular unit of time captures the predominant effect of external variations in conditions (Eq. (7)). Using this temporal scaling ansatz, we derive exact analytic results for how the time-dependent cell age distribution adapts to changing conditions (Eq. (11) and Fig. 2). We derive the natural representation for these time-dependent dynamics in the cell's internal reference frame (Eqs. (6), (7) and Fig. 1). When recast in terms of the new representation, the cell age distribution becomes time-invariant even as growth conditions remain dynamic! (See Fig. 2.) In sum, this result corresponds to the *dynamical* generalization of the previously known scaling law for constant growth conditions. We conclude with a prescription for convenient experimental tests of the proposed temporal scaling ansatz.

Time evolution of the cell age distribution in

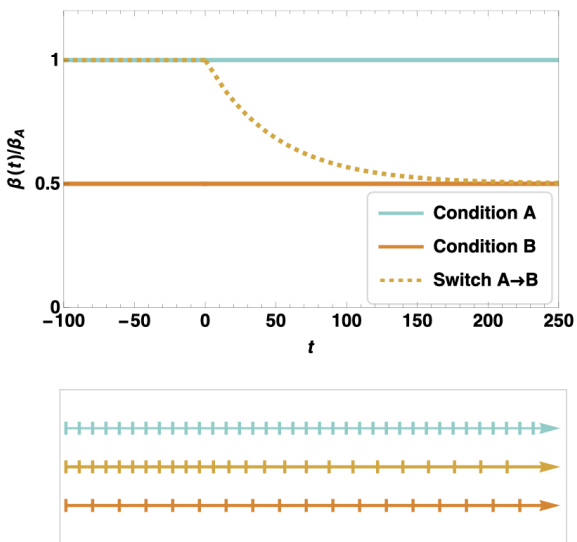

FIG. 1. Schematic representation of the dynamic rescaling of the cellular unit of time. The top panel shows three temporal variations of extrinsic conditions, as encapsulated by the scaling function, $\beta(t)$. Two of these correspond to distinct time-invariant constant growth conditions A and B; the third corresponds to a dynamical switching between these two. The bottom panel shows the 'ticking' of the cellular clock in lab time, color coded in accordance with the top panel. The rescaling, prescribed through Eq. (6), states that at lab time t, the cellular clock runs at an instantaneous rate which is $\beta(t)/\beta(0)$ faster than initially. The 'ticks' of the clock, isochronal in the cell's internal reference frame, are twice as apart in condition B than in A when measured in the lab frame, a reflection of the fact that their scaling factors are related as: $\beta_B = \beta_A/2$. The 'ticks' corresponding to the switch dynamically change their spacing when transitioning between the two conditions, following Eq. (6).

dynamic conditions. First we derive the time evolution equation governing the dynamics of the cell age distribution in time-varying conditions. As ambient conditions change, the timescales of growth and division of individual cells are affected. In turn these changes are reflected in the changing shape of the cell age distribution, $n(t,\tau)$. Here, τ denotes the cell age since the last division event and $n(t,\tau)d\tau$ denotes the number of cells with ages in the range between τ and $\tau + d\tau$ at time t. The total population at time t is thus $N(t) = \int_0^\infty n(t,\tau)d\tau$.

Let $\alpha(t,\tau)$ denote the time-dependent propensity of an individual cell of age τ to give birth to ν daughter cells at time t. Thus, between times t and $t + dt$, $\alpha(t,\tau)n(t,\tau)d\tau dt$ cells with ages in the window between τ and $\tau + d\tau$ will divide and produce ν times as many daughter cells with ages $\tau = 0$. This phenomenology is captured by the temporal evolution equations of the age distribution [13]:

$$(\partial_t + \partial_\tau)n(t,\tau) = -\alpha(t,\tau)n(t,\tau), \tag{1a}$$

$$n(t,0) = \nu \int_0^\infty \alpha(t,\tau)n(t,\tau)d\tau. \tag{1b}$$

The time-dependent propensity also determines the division time distribution for cells born at time t:

$$P(\tau|t) = \alpha(t+\tau,\tau)e^{-\int_0^\tau \alpha(t+\tau',\tau')d\tau'}, \tag{2}$$

where τ is the age at which the cell divides, after being born at time t. Solving Eq. (1a) using the method of characteristics:

$$n(t,\tau) = \begin{cases} n(t-\tau,0)f(t,\tau) & \forall\ \tau < t \\ n(0,\tau-t)\frac{f(t,\tau)}{f(t,\tau-t)} & \forall\ \tau \geq t \end{cases} \tag{3}$$

where

$$f(t,\tau) = e^{-\int_0^\tau \alpha(t-\tau+\tau',\tau')d\tau'} \tag{4}$$

is the probability that a cell born at time $t-\tau$ does not divide before age τ. This is an implicit solution, since the initial condition, $n(0,\tau) \stackrel{\text{def}}{=} n_0(\tau)$, explicitly specifies only the $\tau > t$ case of Eq. (3). The solution for the regime $\tau < t$ in Eq. (3) depends explicitly on the time evolution of newborn cells, $n(t,0) \stackrel{\text{def}}{=} n_B(t)$. To obtain the explicit solution, we express $n_B(t)$ in terms of $n_0(\tau)$ by using Eq. (1b) and Eq. (3), and rewrite as the following implicit equation for $n_B(t)$:

$$n_B(t) = \nu \int_0^\infty \frac{P(\tau+t|-\tau)}{f(t,\tau)} n_0(\tau)d\tau + \nu \int_0^t P(\tau|t-\tau)n_B(t-\tau)d\tau. \tag{5}$$

Upon solving this implicit equation, we can replace $n_B(t)$ by a functional of $n_0(\tau)$ in Eq. (3), thus finding the age distribution, $n(t,\tau)$, in terms of the initial conditions and the general time-dependent division propensity, $\alpha(t,\tau)$.

Temporal scaling ansatz. We next build on the observation that a single timescale, a cellular unit of time, governs stochastic growth and division dynamics under constant growth conditions [12–15]. To characterize cellular dynamics under time-varying conditions, we propose the following temporal ansatz: *The net effect of the variation in growth conditions is simply to rescale the cellular unit of time at each instant.* In other words, the time-dependence of this internal cellular timescale encapsulates the effects of external variations in ambient conditions on the growth and division of individual cells.

Here we focus on theoretical predictions based on the temporal scaling ansatz, while remaining agnostic as to how the scaling factor that scales the internal timescale to match the external (or lab) time, $\beta(t)$, may be calibrated in different experimental setups using conveniently measurable quantities. Evidently, under time-invariant growth conditions, β may be identified with the exponential growth rate of individual bacterial cells [12].

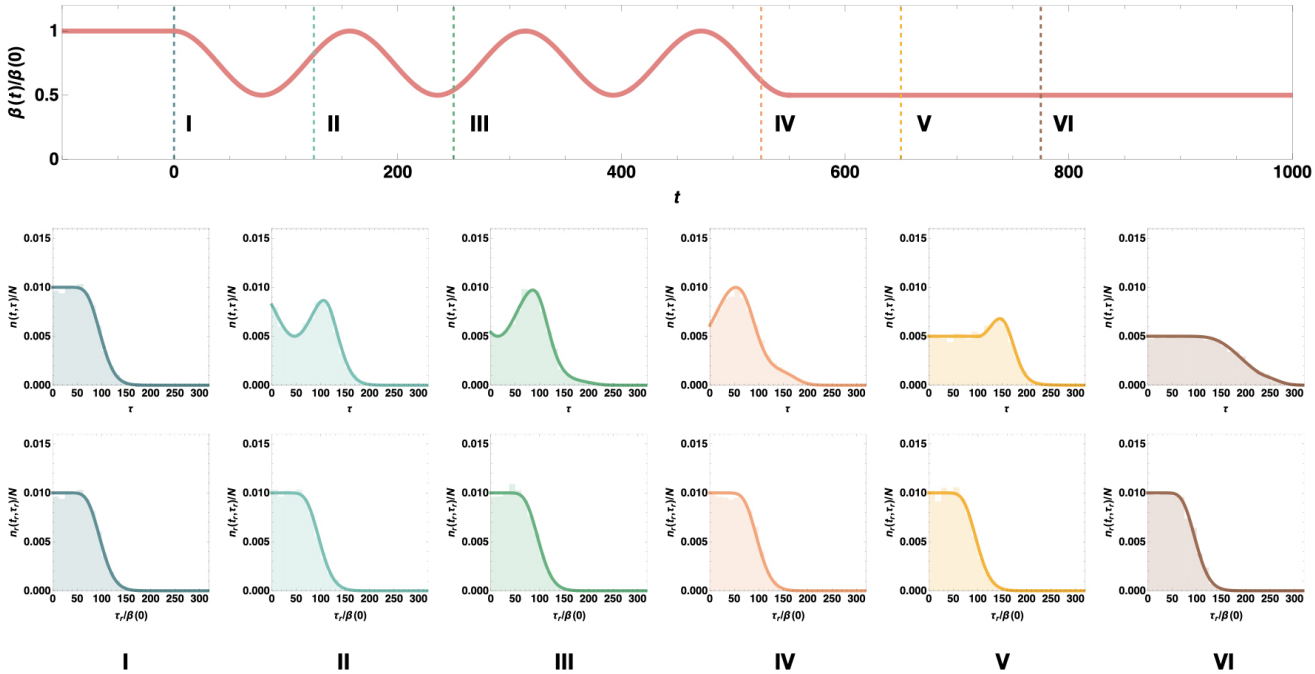

FIG. 2. Evolution of SChemostat age distribution, starting from steady state, under time dependent conditions. The top panel shows a time evolution of the scaling factor, $\beta(t)$, from one constant steady state value to another that is half the starting value, via multiple oscillations. The two bottom rows show the predicted evolution of age distributions, normalized as probability distributions and initially in steady states, corresponding to the time slices $I - VI$ indicated in the top panel. We have taken the division time distribution, in the lab frame and at the initial constant growth condition, to be a Gamma distribution with mean 100 and standard deviation ~ 22; this determines the steady state distributions and the rescaled division time distribution/propensity in the cellular reference frame. The middle row shows age distributions in the laboratory frame, $n(t, \tau)$, while the bottom row shows age distributions in the rescaled internal reference frame of the cell, $n_r(t_r \tau_r)$, where at instant t the cell's internal clock runs at an instantaneous factor of $\beta(t)/\beta(0)$ faster than initially. Each age distribution plot is normalized to 1 and calculated using two complimentary methods: the curve represents the prediction of the analytic procedure presented in this work, and the background histogram was obtained from a complimentary Gillespie simulation of the growth and division of cells for 5000 cells, utilizing division propensities deduced from the assumed steady state division time distribution and $\beta(t)$ (Eqs. (7) and (8)). They match perfectly. The age distribution in the internal frame (bottom row) evolves under time-invariant conditions and thus continues to remain in the steady state it starts from, Eq. (16). The apparently complex time dependence of the lab-measured age distribution (middle row) arises from the time-dependent rescaling action incorporating the history of $\beta(t)$, Eq. (18); under this rescaling, they naturally transition between steady states that are simple rescaled versions of each other.

A natural representation of cellular dynamics in time-varying conditions. The proposed scaling ansatz motivates a natural representation for cellular dynamics in time-varying conditions: the key insight is to instead use the natural dimension-free rescaled variables, transforming from the absolute 'lab time', t, and absolute lab-measured age, τ, of the cell to the corresponding quantities, (t_r, τ_r), measured using the 'internal' clocks of the cells:

$$t_r(t) = \int_0^t \beta(t')dt', \tag{6a}$$

$$\tau_r(\tau, t) = \int_0^\tau \beta(t - \tau + \tau')d\tau' \equiv \int_{t-\tau}^t \beta(t')dt'. \tag{6b}$$

Requiring that the temporal scaling factor $\beta(t)$ always remain positive, these equations uniquely specify (t_r, τ_r) given (t, τ). The implication of the existence of a single (dynamic) governing timescale is that the division propensity, in terms of the intrinsic clock of the cell, is independent of explicit dependence on absolute lab time:

$$\alpha_r(\tau_r) = \frac{\alpha(t, \tau)}{\beta(t)}. \tag{7}$$

It follows that the division time distributions from different constant growth conditions, once mean-rescaled, should undergo a scaling collapse, as is indeed observed in experimental data [12]. The rescaled propensity, $\alpha_r(\tau_r)$, can be expressed in terms of the (static) division time

distribution in the intrinsic cellular frame of reference:

$$\alpha_r(\tau_r) = \frac{P_r(\tau_r)}{\int_{\tau_r}^{\infty} P_r(\tau_r')d\tau_r'}. \tag{8}$$

Upon changing variables, we find that the age distribution in the cellular frame is related to the age distribution in the lab frame as:

$$n_r(t_r, \tau_r) = \frac{n(t,\tau)}{\beta(t-\tau)}, \tag{9}$$

where t, τ are related to t_r, τ_r through Eq. (6). Physically, Eq. (9) implies that to obtain the age distribution in the cellular frame, we need to scale the age distribution in lab frame by the temporal scaling factors at the corresponding times of birth.

Exact solution for the general time-dependent case. In the cellular frame of reference, we find that the age distribution evolves with time as:

$$(\partial_{t_r} + \partial_{\tau_r})n_r(t_r,\tau_r) = -\alpha_r(\tau_r)n_r(t_r,\tau_r) \tag{10a}$$

$$n_r(t_r, 0) = \nu \int_0^{\infty} \alpha_r(\tau_r)n_r(t_r,\tau_r)d\tau_r. \tag{10b}$$

Remarkably, the preceding equation for the time evolution of the age distribution is, in terms of the new variables, identical to that for cells growing and dividing in time-invariant growth conditions [13], a solvable problem! We can thus write down an explicit solution for $n_r(t_r, \tau_r)$ (see below), which can then be used to find $n(t,\tau)$ using Eqs. (9), (7) and (6).

We have derived the solution to Eqs. (10) in SIREF. Starting from an arbitrary initial condition $n_{r,0}(\tau_r)$, the time evolution of $n_r(t_r,\tau_r)$ is given by,

$$n_r(t_r,\tau_r) = \begin{cases} \int_0^{\infty} \frac{f_r(\tau_r)}{f_r(\tau')} F(t_r - \tau_r + \tau')n_{0,r}(\tau')d\tau', & \tau_r < t_r \\ n_{0,r}(\tau_r - t_r)\frac{f_r(\tau_r)}{f_r(\tau_r - t_r)}, & \tau_r \geq t_r \end{cases} \tag{11}$$

where

$$F(\tau) = \mathcal{L}^{-1}\left\{\frac{\nu \hat{P}_r}{1-\nu\hat{P}_r}\right\}(\tau), \tag{12}$$

$\hat{P}_r$ represents the Laplace transform of P_r, and $\mathcal{L}^{-1}$ the inverse Laplace transform operation. $n(t,\tau)$ can now be obtained from $n_r(t_r,\tau_r)$ through Eq. (9) and (6).

Emergent simplicity in temporal evolution under dynamic conditions for growing populations. Since the time evolution in the cellular frame occurs with a constant propensity function $\alpha_r(\tau_r)$ even when growth conditions continue to vary in the lab reference frame, the cell population number, $N(t) \equiv N_r(t_r)$, achieves an exponentially growing steady state for $\nu > 1$. The timescale over which transients die out is $\sim T_{\text{gen}}$, which is the extent of the age distribution, i.e., the timescale corresponding to one cell generation. Thus, for $t >> T_{\text{gen}}$, the total population grows exponentially in the internal cellular reference frame as: $N_r(t_r) = N_0 e^{kt_r}$. The exponential growth rate, k, determined by the condition: $\int_0^{\infty} e^{-k\tau_r}P_r(\tau_r)d\tau_r = 1/\nu$. N_0 is a constant that may not be equal to the initial total population, $N(0)$ and must be found using the full time-dependent solution, Eq. (11). Furthermore, the normalized age distribution in the cellular frame, $n_r(t_r,\tau_r)/N(t_r)$, tends to a steady state limit:

$$n_{SS}(\tau_r) = \frac{k\nu}{\nu-1}e^{-k\tau_r}\int_{\tau_r}^{\infty} d\tau_r' P_r(\tau_r'). \tag{13}$$

Significantly, the asymptotic behavior of n_r determines the time-dependent behavior of the lab-frame age distribution under time-dependent growth conditions:

$$n(t,\tau) \simeq N_0 e^{k\int_0^t \beta(t')dt'}\beta(t-\tau)n_{SS}\left(\int_{t-\tau}^{t}\beta(t')dt'\right), \tag{14}$$

for $t \gg T_{\text{gen}}$ and n_{SS} given by Eq. (13).

Exact evolution of the system when starting from a steady state. Consider the scenario in which the system starts from a steady-state age distribution (for instance after having evolved under a constant growth condition for a sufficiently long period of time) and then experiences a change in conditions leading eventually to a different steady state. Then, at the start of the experiment, the normalized age distribution is already equal to n_{SS} in the cellular reference frame, since the mean-rescaled steady-state age distributions are universal across growth conditions (from the known scaling law for constant growth conditions). Thus, the lab-measured age distribution, even under continuing time-dependent growth conditions, is exactly equal to:

$$n(t,\tau) = N(0)e^{k\int_0^t \beta(t')dt'}\beta(t-\tau)n_{SS}\left(\int_{t-\tau}^{t}\beta(t')dt'\right), \tag{15}$$

where $N(0)$ is the initial cell population number, and n_{SS} is given by Eq. (13).

Emergent simplicity in temporal evolution under dynamic conditions when $\nu = 1$, in a SChemostatic non-growing population. There is practical interest in the case when $\nu = 1$: the mother cell is retained at each division and the daughter cell(s) removed from the experimental arena, resulting in a non-growing constant population number of cells in the experiment. Single-cell technologies such as the SChemostat and the Mother Machine facilitate the experimental realization of this scenario [12, 18–22]. These experiments allow the direct tracking of the age distribution as a function of (lab) time.

When $\nu = 1$, the population is static and so $k = 0$. Compared to the case when $\nu > 1$ (preceding section),

the equation for the normalized steady-state distribution is modified:

$$n_{SS}(\tau_r) = \frac{e^{-\int_0^{\tau_r} \alpha_r(\tau_r')d\tau_r'}}{\langle \tau_r \rangle} \equiv \frac{\int_{\tau_r}^{\infty} P_r(\tau_r')d\tau_r'}{\langle \tau_r \rangle}. \quad (16)$$

We introduce the average division time in the cellular reference frame, $\langle \tau_r \rangle = \int \tau_r P_r(\tau_r) d\tau_r$, to normalize $n_{SS}(\tau_r)$ to 1. Using this and the fact that the total population remains constant at $N(0)$, we have:

$$n(t \gg T_{\text{gen}}, \tau) = \frac{N(0)\beta(t-\tau)}{\langle \tau_r \rangle} \int_{\int_{t-\tau}^{t} \beta(t')dt'}^{\infty} P_r(\tau_r')d\tau_r'. \quad (17)$$

For the special scenario when the population is known to initially begin from a steady state, we no longer need the condition $t \gg T_{\text{gen}}$; the exact solution to the age distribution at all times is:

$$n(t, \tau) = \frac{N(0)\beta(t-\tau)}{\langle \tau_r \rangle} \int_{\int_{t-\tau}^{t} \beta(t')dt'}^{\infty} P_r(\tau_r')d\tau_r'. \quad (18)$$

Illustrative example. Consider the scenario presented in Fig. 2. The rescaling rate $\beta(t)$ is initially constant and both $n(t, \tau)$ and $n_r(t_r \tau_r)$ are in steady state at $t = t_r = 0$. The results compellingly demonstrate our prediction that the rescaled age distribution remains in the expected steady state, Eq. (16), even as the laboratory-measured age distribution transitions from one steady state to a different one following the prediction of Eq. (18).

Prescription for experimental tests of temporal scaling ansatz. The foregoing discussions motivate a convenient prescription for experimental tests of our temporal scaling ansatz. Consider the special scenario when a non-growing population of cells is initialized in some steady state. An advantage of this initialization procedure is that the initial age distribution in the cellular reference frame is then readily known, circumventing the challenge encapsulated in Eq. (6)— in general, it is necessary to know the history of the dynamic scaling function $\beta(t)$ for $t < 0$ to be able to calculate the initial age of a cell. The growth conditions are allowed to vary through the experiment and the age distribution in the lab frame is recorded. The temporal scaling ansatz is validated if a function $\beta(t)$ is found such that upon using it to rescale the observed age distribution according to Eqs. (6) and (9), the resulting distribution, $n_r(t_r, \tau_r)$, becomes time-invariant.

Concluding remarks. The issue of how homeostasis in growth and division of individual cells is sustained in constant growth conditions has received considerable attention[18, 23, 24]. The framework we have developed here can serve as a useful starting point for extensions to time varying growth conditions, and conditions in which cells are intermittently subjected to stress [4–8]. Recently, the issue of computation without neurons has received increasing attention [25–28]. Our recent work shows that cell size does not serve as repository of memory [18, 24]. This work could also serve as a useful starting point for understanding memory formation and retention when time varying growth conditions are involved.

In this theoretical work, we have remained agnostic as to the specific identify of the dynamic scaling factor, $\beta(t)$. What observable timescale does it correspond to? We believe that the specifics of the biology of the cells and the experimental setup used become important for correct identification of this dynamic timescale. Even for the reasonably circumscribed case of individual bacterial cells in microfluidic platforms designed to prevent 2 and 3 dimensional crowding, individual cells in different setups experience dynamic changes in conditions differently. For example, in the popular mother-machine-based approaches [5, 6, 19–22], the desired change in conditions has to be implemented in the main feeding channel, whereas the response of interest is that of the mother cell at the far end of the perpendicular trapping trench, to where nutrients from the feeding trench must arrive after passing around a line of tightly packed newer-born daughter cells. So precisely what temporal changes the mother cell experiences and with what delay may need to be calibrated from experiment to experiment and replicate to replicate. However, we believe that these experimental challenges are surmountable and direct tests of the predictions made here will be shortly forthcoming.

AUTHOR CONTRIBUTIONS

R.R.B. and S.I.-B. conceived of and designed the research; K.J., S.R., R.R.B. and S.I.-B. performed analytic calculations; K.J. performed numerical computation and simulations under the guidance of S.I.-B.; K.J., R.R.B., and S.I.-B. wrote the paper; S.I.-B. supervised the research.

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ORIGINALITY STATEMENT

This work represents human endeavor; we did not use AI-based chatbots to generate the research content or the prose.

APPENDIX

Transient Age Distribution in Intrinsic Cellular Frame of Reference

From the noted scaling laws, solving for the age distribution in the intrinsic cellular frame of reference is equivalent to solving for a system in which division propensity is independent of time, i.e., Eq. (1) under the condition that α is independent of time t. Thus,

$$n_r(t_r,\tau_r) = \begin{cases} n_{B,r}(t_r-\tau_r)f_r(\tau_r) & \forall\ \tau_r < t_r \\ n_{0,r}(\tau_r-t_r)\frac{f_r(\tau_r)}{f_r(\tau_r-t_r)} & \forall\ \tau_r \geq t_r \end{cases} \tag{19}$$

where $n_{0,r}$ is the given initial age distribution in the intrinsic cellular frame of reference, and

$$f_r(\tau_r) = e^{-\int_0^{\tau_r}\alpha_r(\tau')d\tau'}, \tag{20}$$

and, similarly to Eq. (5), we have,

$$\begin{aligned} n_{B,r}(t_r) =& \nu\int_0^\infty \frac{P_r(\tau+t_r)}{f_r(\tau)}n_{0,r}(\tau)d\tau \\ &+\nu\int_0^{t_r} P_r(\tau)n_{B,r}(t-\tau)d\tau. \end{aligned} \tag{21}$$

Applying Laplace transform to the above equation,

$$\frac{\hat{n}_{B,r}(s)}{\nu} = \int_0^\infty \frac{e^{\tau s}}{f_r(\tau)}\hat{P}_r(s)n_{0,r}(\tau)d\tau + \hat{n}_{B,r}(s)\hat{P}_r(s), \tag{22}$$

$$\Rightarrow \hat{n}_{B,r}(s) = \int_0^\infty \frac{e^{\tau s}}{f_r(\tau)}n_{0,r}(\tau)d\tau\frac{\nu\hat{P}_r(s)}{(1-\nu\hat{P}_r(s))}. \tag{23}$$

Taking the inverse Laplace transform, we get,

$$n_{B,r}(t_r) = \int_0^\infty \frac{1}{f_r(\tau)}\mathcal{L}^{-1}\left\{\frac{\nu\hat{P}_r}{1-\nu\hat{P}_r}\right\}(t_r+\tau)n_{0,r}(\tau)d\tau. \tag{24}$$

Replacing this in Eq. (19) yields Eq. (11).

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