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Addressing the Division Clock:

Codon Gating at the Membrane, the Reusable X-A Catalyst, and the Set Point of the Lineage

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Abstract. The three preceding articles concluded that at a fixed line of their loop the lineage divides once per forcing period whatever the condensation rate. With the division reset applied, no dividing vessel is born on that line: division in one cycle requires no net growth, and a lineage held there reaches the dilution floor in 39.5 generations at $\alpha = 0.10$. While the osmolyte input is proportional to the particle count, no membrane-limited condensation law linear or saturating in the remnant sets a size.

The input is therefore changed. Lipids arrive as a per-cycle flux tied to genome length, one lipid to a pair of units. Genome hexamers `AAA` and `TTT` template the tethered adenosine–chrysene triplet `X-A X-A X-A` in the bilayer, as in the patent record. Codons expressed on lipid-tethering events excise its middle unit; the flanking units reform and serve again, and condensation runs at the same units.

Under named hypotheses the catalyst density is the root of a quadratic; the bud is born with osmolyte per lipid equal to the mother's free remnant per lipid at division, $R_{\mathrm{bud}} = R_0\, w_{\mathrm{div}}/u_0$; the period is the time to regrow one bud's lipids, equal to the forcing period exactly when one cycle's lipids close one bud; and without condensation every mother line converges for bud fractions below one half. The mother line's bud is the largest of a distribution: at the baseline three births in four fall below the floor, a fraction fixed by lineage structure, and a population with every birth viable needs about twice the mother line's input. A gate mixing tethering events with standing membrane keeps the set point locally, in a basin that the basal share bounds and condensation widens. Under one codon per event the viability conditions become conditions on the sequence, which a random 200-unit genome meets at most one time in five. The sequence content sets the scale of the size distribution; the genome length sets the period. Corrections to the preceding articles are recorded as precedence rulings.

Keywords: encoder; codon gating; lipid tethering; registry hexamer; reusable catalyst; remnant gauge; division period; size set point; hybrid dynamics; precedence; Chrysene Formalism

1 Introduction

Article 67 composed the pore, the photoentrained cycle and the material ledger, and found that the remnant of the excision accumulates in the bilayer at the rate the osmolyte is made. Article 68 supplied a condensation edge that sequesters the remnant and set the rate condition $f_c \geq \beta$. Article 69 found a fixed line of the resulting per-cycle map, at which $f_c = \beta$, N is constant and the division period equals the forcing period T for every α and every rate constant k. It closed with a target, `tgt:encoder`: whether the genome sets k, and through it the amplitude of the loop without touching its period.

1.1 What this article finds

The fixed line is a property of the per-cycle map alone. Once the division reset is applied, no dividing vessel is born on it (Section 4). The attractor of the system as written divides in $\tau(\alpha)$ cycles, not one, whatever the condensation law, and its size is fixed by the condensation constant. Under an osmolyte input proportional to the particle count, however, no condensation law limited by a fixed number of membrane sites and linear or saturating in the remnant gives a stable size (Section 5). The mandate of `tgt:encoder` cannot be met on that input.

The input is therefore changed (Sections 6 and 7). Lipids arrive as a per-cycle supply tied to the genome. Residues arrive through codons expressed on lipid-tethering events and accepted at a reusable `X-A` catalyst that the genome's `AAA` and `TTT` hexamers supply. On that loop the bud size is gauged exactly by the remnant, the period is exactly the time to make one bud's lipids, and both are set by the genome (Section 10). The set point is first that of a mother line; Section 8 places it in the population it belongs to, proves convergence where it can, and finds the population's viability threshold twice the mother line's. Section 9 turns the gate hypothesis into a tolerance, and Section 10.1 turns the unknown constants into conditions on the

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sequence.

1.2 What is established here, by kind

Proved here. That one-cycle division requires no net growth (Lemma 4.1); that $W_b - N$ is invariant for every condensation law (Proposition 4.2); the period of the size-stationary line of the earlier system (Theorem 4.3); that L_{lip} is a per-cycle supply (Proposition 6.1); the catalyst density (Proposition 7.3); the remnant gauge (Theorem 7.4); the period identity (Theorem 7.5); the ceiling (Proposition 7.6); the two extreme lines (Proposition 8.2); global convergence of every mother line without condensation for $\alpha < 1/2$ (Theorem 8.3); and the sequence and supply bounds (Propositions 10.6, 10.10).

Computed here. The attractors, set points, founder independence, the effect of genome length, the reuse comparison, the collapse under the stock gate, the population distribution and its viability thresholds, local stability where the proof does not reach, the tolerance of the mixed gate, and what random and enriched genomes supply. Appendix B.

Supposed. The ten hypotheses of Sections 2.1 and 10.1, of which the gate (Hypothesis 2.8) is the one the set point turns on.

Not claimed. Everything in Section 3.

1.3 Organization

Section 2 fixes status, conventions and the hypothesis register; Section 3 states the non-implications. Section 4 analyses the system of Articles 67–69 with division included; Section 5 shows why its input had to change. Section 6 reads the lipid supply and the registry hexamer; Section 7 defines the loop and proves its identities; Section 8 treats the population and convergence; Section 9 the gate as a tolerance; Section 10 states what the genome sets and bounds the parameters; Section 11 what condensation does. Section 12 carries the registers, the precedence rulings, the targets and the conclusion. Appendix A is the hypothesis register, Appendix B the verification, Appendix C the correction ledger.

2 Status, conventions, hypotheses

Convention 2.1 (Status labels)**.** [A] As in the coordinating paper: [A] finite or axiom-free; [D] derived under named hypotheses, registered in Appendix A; [C] imported, with the source named; [E] molecular reading, which enters no proof. Scholia carry no label and enter no proof. A statement marked *computed* is a finite computation emitted by a block of Appendix B and is not proved.

Convention 2.2 (The reset)**.** [A] The division reset produces two taut daughters and conserves area. Lumen species split in the ratio $\alpha : 1-\alpha$. Membrane species, namely lipids Λ, free remnant W_b, sequestered remnant W_s, co-aggregate P and catalyst X, split by area share,

$$b_A = \frac{\alpha^{2/3}}{Q(\alpha)} \text{ (bud)}, \qquad s_A = \frac{(1-\alpha)^{2/3}}{Q(\alpha)} \text{ (mother)},$$

with $b_A + s_A = 1$. Block X1a shows that the reset as transcribed in Articles 67 and 69, $(\alpha N, \alpha^{2/3}A)$, leaves the bud at $v_{\text{thr}}(\alpha)$ rather than at 1 and sums the daughter areas to $Q(\alpha)A$.

Convention 2.3 (Two readings of one map)**.** [A] The *per-cycle reading* tests $v \le v_{\text{thr}}(\alpha)$ at the end of each cycle, as Articles 67–69 do. The *continuous reading* treats per-cycle fractions as rates per T and divides at the first crossing of $v_{\text{thr}}(\alpha)$. Statements hold in both unless one is named.

Notation 2.4 (Symbols)**.** [A] N lumen osmolyte; W_b free remnant; Λ lipid count, area $A = \Lambda a/2$ with $a = 0.65$ nm^2; X catalyst X-A units; $u = N/\Lambda$, $w = W_b/\Lambda$, $x = X/\Lambda$. The founder has $R_0 = 100$ nm, $\Lambda_0 = 386{,}658$ lipids and $u_0 = N_0/\Lambda_0 = 0.6517$ (block X6). λ is lipids supplied per cycle. A taut vessel has $v = 1$ and radius $R = R_0\,(\Lambda/\Lambda_0)^{1/2}$.

2.1 The hypothesis register

The first two hypotheses fix the setting; the next five define the loop; the last two are carried from earlier articles in a named form.

Hypothesis 2.5 (One strand)**.** [D] A vessel carries one genome strand of L encoded units, anchored to the inner leaflet as in Article 62, Section 8. Registered as H1.

Hypothesis 2.6 (Genome-tied lipid supply)**.** [D] Lipids enter the membrane at $\lambda = \nu L/2$ per cycle: ν unrecruited units per encoded unit (Article 62, Theorem 10.5), one lipid to a pair of substituted chrysenes (U.S. Patent 12,195,423; Article 62, Proposition 10.2). Registered as H2.

Hypothesis 2.7 (The triplet)**.** [D] Genome hexamers of registry class 00000 template the triplet complex X-A X-A X-A, A an adenosine and X the chrysene tethered to it, at π copies per template per cycle. The complex is integrated in the phospholipid bilayer as in U.S. Patent 12,195,423, Figures 15A, 15B, 15C and 20. Each copy brings three X-A units to the

membrane. Registered as H3.

Hypothesis 2.8 (The gate)**.** [D] Codons of the genome are expressed at $E = \eta\lambda$ per cycle: expression is triggered by each lipid-tethering event, the tethering of the membrane to the genome having been established in the synthesis phase (U.S. Patent 12,195,423). The trigger is the event, not the tethered stock; a basal share proportional to the stock is admitted in Section 9. Registered as H4.

Hypothesis 2.9 (Acceptance by class)**.** [D] A codon of registry class O is accepted at a reformed `X-A` tether with probability $a(O)$. The accepted fraction is

$$\Phi_G = \sum_{O \in X} \mu_G(O)\, a(O),$$

μ_G the class distribution of the genome's codons. Registered as H5.

Hypothesis 2.10 (The site cycle)**.** [D] An accepted codon excises the middle `X` of a three-unit `X-A` tether: one residue to the lumen, one remnant to the bilayer, one `X-A` unit consumed. The flanking units are not excised; they reform with adjacent poly `X-A` and accept further codons. Acceptance saturates in the catalyst with half-saturation density K per lipid. Registered as H6.

Hypothesis 2.11 (Condensation at the catalyst)**.** [D] Condensation runs at the `X-A` units at $F = c\, X\, W_b/\Lambda$: first order in the catalyst and in the free remnant per lipid. Registered as H7. It replaces Hypothesis H1 of Article 68.

Hypothesis 2.12 (One-to-one sequestration)**.** [D] Each condensed residue sequesters one remnant ($\varepsilon = 1$), as Article 68 assumed without naming it. Registered as H8.

Hypothesis 2.13 (Base to letter)**.** [D] The datum of Article 62, Definition 4.7, written here $(\alpha_{62}, \beta_{62})$ to keep it apart from the bud fraction α and from $\beta = \alpha/(1-\alpha)$, is the pair (b_1, b_2) of Article 45, Definition 3.12, read at frame $f = 0$: $\mathtt{A} \mapsto FF$, $\mathtt{T} \mapsto BB$, $\mathtt{C} \mapsto BF$, $\mathtt{G} \mapsto FB$. Registered as H9.

Remark 2.14 (What the gate hypothesis carries)**.** [A] Hypotheses 2.6–2.11 each fix a figure. Hypothesis 2.8 fixes whether there is a set point at all: with the gate on the tethered stock instead of the tethering event, the lineage collapses (Proposition 7.12). Section 9 measures how much stock the gate can carry. It is the premise to settle first.

3 Non-implications

Proposition 3.1 (Non-implications)**.** [A] *None of the following is asserted below.*

(i) That the acceptance of codons by class is a genetic code. *No residue identity is assigned to any class. Article 45, Proposition 3.15, stands: its surjection of sixty-four words onto twenty classes is not the standard code.*

(ii) That any parameter is known. *η, $a(\cdot)$, π, K and c are not supplied by the corpus. Figures computed at stated values are illustrations of the identities, not predictions.*

(iii) That the set point is viable at the stated values. *At the baseline the mother line's bud lies below the dilution floor (Remark 7.10), and so do three births in four (Proposition 8.5).*

(iv) That a mother line describes the population. *Its bud is the largest the loop makes (Scholium 8.7).*

(v) That condensation relieves the bilayer. *Section 11 shows the opposite.*

(vi) That the phenotype is regulated. *The genome specifies a set point; nothing here responds to conditions.*

(vii) That the fixed line of Article 69 is reached. *Corollary 4.4.*

(viii) That the residue reaches the lumen. *Its route from the membrane site to the lumen is assumed in Hypothesis 2.10, not shown.*

4 The earlier system with division included

This section takes the system of Articles 67–69 as written: input βN per cycle, area growth by $Q(\alpha)$ per cycle, linear condensation $f_c = kW_b/L_{\text{lip}}$ with L_{lip} a per-vessel constant, and the reset of Convention 2.2, applied to lumen and remnant alike as Article 67 did.

Lemma 4.1 (One-cycle division requires no net growth)**.** [A] *Let a vessel be born at $v = 1$ with $\gamma_0 = \beta - f_c(W_b)$ at birth.*

After one cycle $v_1 = (1+\gamma_0)Q(\alpha)^{-3/2}$, *so*

$$v_1 \le v_{\text{thr}}(\alpha) \iff \gamma_0 \le 0 \iff N_1 \le N_{\text{birth}}.$$

A mother line dividing every cycle therefore keeps at most a fraction $1-\alpha$ *of its particles per generation, and reaches* $R_{\min} = 25$ *nm from* $R_0 = 100$ *nm in at most* $3\ln 4/\ln\big(1/(1-\alpha)\big)$ *generations:* 39.5, 81.1 *and* 205.9 *at* $\alpha = 0.10$, 0.05, 0.02. *Block X1b.*

Proof. On the per-cycle map $N_1 = N_{\text{birth}}(1+\gamma_0)$ and $A_1 = Q(\alpha)A_{\text{birth}}$; substitute in $v = (N/N_{\text{birth}})(A/A_{\text{birth}})^{-3/2}$ and compare with $v_{\text{thr}}(\alpha) = Q(\alpha)^{-3/2}$. The mother carries $(1-\alpha)N_1 \le (1-\alpha)N_{\text{birth}}$ forward, and a taut radius scales as $N^{1/3}$. □

Proposition 4.2 (The invariant $W_b - N$). 🄰 *For every condensation law,* $D = W_b - N$ *is invariant under the per-cycle map, because* N *and* W_b *receive the same increment* $\gamma_k N_k$ *(Article 69, Remark (equal increments)). A reset that splits both in the ratio* $\alpha : 1-\alpha$ *multiplies* D *by* α *or* $1-\alpha$, *so along a mother line* $D_g = (1-\alpha)^g D_0 \to 0$ *and* $W_b/N \to 1$ *at division. Block X1c checks invariance under linear, saturating and step laws.*

Theorem 4.3 (The size-stationary mother line). 🄳 *In the continuous reading a mother line whose particle count at birth is the same in every generation divides with period*

$$\tau(\alpha) = 1 + \frac{2}{3}\,\frac{\ln\big(1/(1-\alpha)\big)}{\ln Q(\alpha)} \text{ cycles},$$

1.5102, 1.3517 *and* 1.2300 *at* $\alpha = 0.10$, 0.05, 0.02, *whatever the condensation law. Under the linear law its particle count at division is* $N_{\text{div}} = u^*(\alpha)L_{\text{lip}}/k$ *with* $u^* = 0.0435$, 0.0151, 0.0040. *In the per-cycle reading the period is* 2 *cycles. Blocks X1d, X1e.*

Proof. Size stationarity requires growth by $1/(1-\alpha)$ per generation, so $v(\tau) = (1-\alpha)^{-1}Q(\alpha)^{-3\tau/2}$; equating to $Q(\alpha)^{-3/2}$ gives $\tau(\alpha)$. On $D = 0$ the variable kN/L_{lip} is logistic with rate β; requiring it to return to its value at division over $\tau(\alpha)$ from $1-\alpha$ times that value gives u^* in closed form (block X1e). □

Corollary 4.4 (The fixed line is not occupied). 🄳 *A vessel born on the fixed line of Article 69 divides after one cycle without net growth, so a lineage held there is bounded by Lemma 4.1. Computed: from the founder at* $\alpha = 0.10$, $k = 0.05$, *every division is followed by* $\gamma_0 > 0$, *and over the attractor grid no generation lasts one cycle. Block X1d.*

Remark 4.5 (What the earlier system does). 🄰 Computed, block X1e: the earlier system converges to the line of Theorem 4.3, with $W_b = N$ at division and a size set by k. Its period does not depend on k, as Article 69 required, but the reason is size stationarity and not the identity $v_{\text{thr}}(\alpha)Q(\alpha)^{3/2} = 1$, and the period is $\tau(\alpha)$ and not T.

5 Why the input had to change

Suppose condensation is limited by a fixed number of membrane sites, $n_m = \sigma L$, at rate $F = \kappa n_m W_b/L_{\text{lip}}$, with the input still βN.

Proposition 5.1 (The genome length cancels). 🄰 *With* $L_{\text{lip}} = \nu L$ *the per-capita condensation is* $(\kappa\sigma/\nu)(W_b/N)$: *the length* L *does not enter. Block X2.*

Theorem 5.2 (The stability of a size set point). 🄳 *On the attractor* $W_b = N$, *let* $\phi(N)$ *be the per-capita condensation. A fixed point of the birth-size map, where one exists, is stable if* ϕ *is increasing, neutral if* ϕ *is constant, and unstable if* ϕ *is decreasing. Existence needs a range condition on* ϕ *that is not supplied here. Computed slopes of the birth-size map at* $\alpha = 0.10$: *linear law with fixed* L_{lip}, 0.9100 *(stable); fixed sites with fixed* L_{lip}, 1.0000 *(neutral); fixed sites with lipids proportional to area,* 1.0649 *(unstable); saturating,* 1.0496 *(unstable); cooperative of order four with lipids proportional to area,* 0.9691 *(stable). Block X3.*

Proof. The log-growth over a generation is $\Gamma(N_b) = \frac{3}{2}\ln Q(\alpha)\,(t_d - 1)$. A larger vessel with ϕ increasing grows more slowly at every instant, by comparison of solutions of a scalar equation, so crosses $v_{\text{thr}}(\alpha)$ earlier and grows less; Γ decreases and the birth-size map has slope below one. The other two cases are the same argument with the inequality reversed or absent. The argument concerns the slope at a fixed point and says nothing of its existence. □

Corollary 5.3 (A drift, not a size). 🄳 *With fixed membrane sites and a concave flux, the genome sets the per-capita condensation* c *and therefore the drift of size across generations. Size holds only at* $c^* = 0.0413$, 0.0147, 0.0040 *for* $\alpha = 0.10$, 0.05, 0.02. *From the founder with* L_{lip} *read as the corpus wrote it, the load exceeds five per lipid from generation 11 whatever* c *is near* c^*. *Block X4.*

Scholium 5.4 (The source of the difficulty)**.** The input βN is proportional to the particle count, so a larger vessel makes osmolyte faster in proportion. A size set point then needs a condensation that grows faster than in proportion, which a fixed number of sites cannot supply. The remedy taken below is on the input: supplies that are fluxes set by the genome, not rates proportional to the vessel's own contents.

Remark 5.5 (What survives the correction of L_{lip})**.** [A] Sections 4–5 analyse the earlier system as written, with L_{lip} a standing count, which Proposition 6.1 corrects. Lemma 4.1, Proposition 4.2, the period of Theorem 4.3, Proposition 5.1 and Theorem 5.2 do not depend on the value of L_{lip} and survive the correction. The sizes of Theorem 4.3 and the load figure of Corollary 5.3 do depend on it and describe the earlier system only.

6 The lipid supply and the registry hexamer

Proposition 6.1 (L_{lip} is a per-cycle supply)**.** [D] *In Article 67's transcription of the allocation of Article 65 (block V1), the lipid entry* 13,200 *sits in one pool with* 28,000 *residues per cycle and* 1,000 *anchor units, the pool being their sum,* 42,200*. Only the residue column is marked per cycle; that the lipid entry is per cycle is an inference from the sum, and it is the reading taken here. At one lipid to a pair of units (Hypothesis 2.6) it is* 6,600 *lipids per cycle, which close a vesicle of* 13.06 *nm, the model-2 radius of Article 62 about a* 200*-unit strand. The founder of* $R_0 = 100$ *nm carries* 773,315 *units,* 58.6 *times as many. Block P1l.*

Proof. Arithmetic on the allocation as transcribed, with Article 62, Definition 10.1, $N(R) = 8\pi R^2/a$, at $a = 0.65$ nm^2, together with the inference named in the statement. Article 65 itself is not consulted (Target 12.14). The other reading puts the founder below its own dilution floor. □

Remark 6.2 (Consequence)**.** [A] Read as a standing count, L_{lip} makes every load W_b/L_{lip} of Articles 67–69 too large by the factor 58.6; read as a supply, it makes the membrane a state Λ fed at λ. The second reading is taken here, and Ruling 67.7 records the correction.

Definition 6.3 (Registry hexamer, codon, triplet)**.** [A] A *registry hexamer* is a six-site stack of Article 45, three vessels, here three consecutive encoded units of the strand. Read in non-overlapping triplets from the first unit, the strand carries $\lfloor L/3 \rfloor$ hexamers, its *codons*, each in one of the twenty frame classes of Article 45, Theorem 3.3. The *triplet* is the post-genome complex of Hypothesis 2.7.

Proposition 6.4 (The triplet's class)**.** [D] *Under Hypothesis 2.13 the sixty-four codons fall into twenty classes, eight of two codons and twelve of four, as Article 45, Corollary 3.7, requires. Three consecutive adenosine-tethered units on one strand read* `AAA`*, and on the other strand* `TTT`*; both lie in the class* `00000`*, the constant-registry class of Article 45, Appendix A, row 1, of size two and stabiliser type r. No other codon lies in it. Block X5.*

Remark 6.5 (A wider reading)**.** [A] If an adenosine tether on either strand qualified, the codons whose three pairs are all of the adenine type would count: eight words in the three classes `00000`, `00010` and `01010`. The narrower reading is the one Hypothesis 2.7 names.

Definition 6.6 (Genome gain and catalyst supply)**.** [A] With μ_G the class distribution of the codons and $n_A = \mu_G(\texttt{00000})\lfloor L/3 \rfloor$ the number of templates,

$$\iota = \eta\,\Phi_G, \qquad \pi' = \frac{\pi n_A}{\lambda} = \frac{2\pi\,\mu_G(\texttt{00000})}{3\nu}.$$

ι is codons accepted per lipid supplied; π' is triplets supplied per lipid. Neither depends on L.

Remark 6.7 (The functional of Article 45)**.** [A] Φ_G is the functional of Article 45, Definition 6.6, with the ensemble the genome's codon classes and the weight the acceptance table. Classes are frame invariant, so Φ_G is a quantity of the assembly in the sense of Article 45, Theorem 3.3(iii). Neither Target 7.5 nor Target 7.6 of Article 45 is discharged: $a(\cdot)$ is supplied by hypothesis, and μ_G is the composition of one strand, not a measure supplied by the axioms.

7 The loop

Definition 7.1 (The loop)**.** [D] Under Hypotheses 2.5–2.12, between divisions and per cycle T,

$$\dot\Lambda = \lambda, \qquad J = \iota\lambda\,\frac{X}{X + K\Lambda},$$
$$\dot X = 3\pi'\lambda - J, \qquad F = c\,X\,\frac{W_b}{\Lambda},$$
$$\dot N = \dot W_b = J - F, \qquad \dot W_s = \dot{\mathrm{P}} = F,$$

with division at $v = (N/N_0)(\Lambda/\Lambda_0)^{-3/2} = v_{\mathrm{thr}}(\alpha)$ and the reset of Convention 2.2. The genome enters through three fluxes, each proportional to L: lipids λ, triplets $\pi'\lambda$, and accepted codons $\iota\lambda$.

Remark 7.2 (Where each piece of the corpus sits). E The residue is Article 67's osmolyte, now made at the membrane; the remnant is Article 67's `W`; condensation is Article 68's edge, now at the `X-A` units rather than at the hexameric ring of the loom papers; the division threshold and the area-conserving reset are Article 64's; the lipid and the strand anchoring are Article 62's; the codon classes are Article 45's. Nothing in the loop is new except the coupling.

7.1 Exact statements

Proposition 7.3 (Catalyst density). D *Under Hypotheses 2.6, 2.8 and 2.10, $x = X/\Lambda$ obeys*

$$\dot{x} = \frac{\lambda}{\Lambda}\Big[\,3\pi' - \iota\,\frac{x}{x+K} - x\Big],$$

which involves no other state, and the reset multiplies X and Λ by the same share. Hence $x \to x^*$, the positive root of

$$x^{*2} + (K + \iota - 3\pi')\,x^* - 3\pi' K = 0,$$

from every initial state, and the realized input per lipid is $\iota_{\mathrm{eff}} = \iota\,x^*/(x^*+K) \le \iota$. The pool is maintained iff $3\pi' > \iota_{\mathrm{eff}}$.

Proof. Divide $\dot{X}$ by Λ and subtract $x\dot{\Lambda}/\Lambda$. The bracket is strictly decreasing in x, positive at 0 and negative for large x, so its zero is unique and attracting; the time change $ds = (\lambda/\Lambda)dt$ does not alter that. The area-split reset preserves x. □

Theorem 7.4 (The remnant gauges the bud). D *On a size-stationary mother line of any loop in which $\dot{N} = \dot{W}_b$ (one residue and one remnant per excision, Hypothesis 2.10; one remnant sequestered per condensed residue, Hypothesis 2.12) and the reset is that of Convention 2.2, the bud is born with osmolyte per lipid equal to the mother's free remnant per lipid at division, $u_{\mathrm{bud}} = w_{\mathrm{div}}$, and*

$$R_{\mathrm{bud}} = R_0\,\frac{w_{\mathrm{div}}}{u_0}.$$

Proof. Over a stationary generation the mother's N rises from $(1-\alpha)N_d$ to N_d and its W_b from $s_A W_d$ to W_d; the increments are equal, so $\alpha N_d = b_A W_d$. The bud receives αN_d and $b_A\Lambda_d$, hence $u_{\mathrm{bud}} = W_d/\Lambda_d = w_{\mathrm{div}}$. A taut bud with $N = u\Lambda$ satisfies $(u/u_0)(\Lambda/\Lambda_0)^{-1/2} = 1$, so $\Lambda_{\mathrm{bud}} = \Lambda_0(w_{\mathrm{div}}/u_0)^2$ and the radius follows from Notation 2.4. □

Theorem 7.5 (The period identity). D *Under Hypothesis 2.6, on the same line the period is the time to regrow one bud's lipids,*

$$\tau = \frac{\Lambda_{\mathrm{bud}}}{\lambda} = \Big(\frac{R_{\mathrm{bud}}}{R_{62}}\Big)^2, \qquad R_{62}^2 = \frac{a\nu L}{16\pi},$$

R_{62} the radius that one cycle's lipids close (Article 62, Definition 10.1). The period equals T exactly when one cycle's lipids close one bud. At $\nu = 66$, $L = 200$: $R_{62} = 13.06$ nm. Blocks X6, P1l.

Proof. The mother's Λ rises from $s_A\Lambda_d$ to Λ_d at rate λ, so $\tau = b_A\Lambda_d/\lambda = \Lambda_{\mathrm{bud}}/\lambda$; substitute $\Lambda = 8\pi R^2/a$ and $\lambda = \nu L/2$. □

Proposition 7.6 (The ceiling). D *Under Hypotheses 2.10 and 2.11, with $x = x^*$, $\dot{w} = (\lambda/\Lambda)(\iota_{\mathrm{eff}} - w) - c\,x^* w$, so $w < \iota_{\mathrm{eff}}$ whenever it starts below, as it does from the founder ($W_b = 0$), and $R_{\mathrm{bud}} < R_0\,\iota_{\mathrm{eff}}/u_0$ for every c. A bud above the dilution floor therefore requires $\iota_{\mathrm{eff}} \ge u_0 R_{\min}/R_0 = 0.1629$ (block X6).*

Remark 7.7 (Article 69's identity, in its new form). A Article 69 found the period equal to T because the area was assumed to grow by exactly one division's worth per cycle. Theorem 7.5 replaces the assumption with a statement: the period is T when the lipid flux the genome supplies per cycle is one bud's membrane. The equality is now a condition that can fail, with the amount by which it fails given by $(R_{\mathrm{bud}}/R_{62})^2$.

Remark 7.8 (The stipulation in ν). A $\nu = 66$ is Article 62's value at a stipulated bending tolerance, over a range of 22–219. By Theorem 7.5, $\tau = 16\pi R_{\mathrm{bud}}^2/(a\nu L)$, so at fixed bud size every period in this article scales as $1/\nu$ and carries that stipulation.

7.2 Computed statements

The baseline is $\alpha = 0.10$, $\iota = 0.2$, $\pi' = 0.08$, $K = 0.02$, $c = 0.05$, $\nu = 66$, $L = 200$.

Proposition 7.9 (The set point)**.** [D] *Computed, block X9, following the mother at every division: the mother lines of founders of* 30*,* 100 *and* 300 *nm converge to one orbit, with bud radius* 23.147 *nm and period* 3.1388 *cycles. At the baseline* $x^* = 0.0800$ *and* $\iota_{\text{eff}} = 0.1600$*, so the ceiling of Proposition 7.6 is* 24.5 *nm. The bud radius and the free remnant at division agree with Theorem 7.4 to the printed precision. Against c:*

c	τ	R_{bud} *(nm)*	w_{div}	*burden*
0.00	*3.531*	*24.55*	*0.1600*	*0.240*
0.05	*3.139*	*23.15*	*0.1509*	*0.249*
0.10	*2.863*	*22.11*	*0.1441*	*0.256*
0.20	*2.485*	*20.59*	*0.1342*	*0.266*
0.50	*1.893*	*17.97*	*0.1171*	*0.283*
1.00	*1.449*	*15.73*	*0.1025*	*0.297*

The burden is free and sequestered remnant, co-aggregate and catalyst, per lipid.

Remark 7.10 (Below the floor)**.** [A] The baseline bud, 23.147 nm, lies below $R_{\min} = 25$ nm, and so does the ceiling, 24.5 nm, because $\iota_{\text{eff}} = 0.1600 < 0.1629$. Viability needs a slightly larger accepted fraction or catalyst supply. The baseline was not tuned to pass, and is reported as computed. The population fares worse than the mother line (Corollary 8.6).

Proposition 7.11 (Reuse)**.** [D] *Computed, block X9: at* $\iota = 0.2$ *and* $c = 0.05$ *the single-use variant, in which each triplet supports one excision and remains as a site, needs* 0.200 *triplets per lipid and stands at* 0.432 *per lipid of burden, with bud* 25.82 *nm and period* 3.905 *cycles; the loop of Definition 7.1 needs* 0.080 *triplets per lipid and stands at* 0.249*, with bud* 23.15 *nm and period* 3.139*. Excisions per triplet are* 2.00 *at* $\pi' = 0.08$ *and rise toward three only as the supply falls toward* $\iota_{\text{eff}}/3$ *and the catalyst depletes:* 2.14 *at* $\pi' = 0.07$*,* 0.95 *at* $\pi' = 0.20$*.*

Proposition 7.12 (The gate must be the event)**.** [D] *Computed, block X9(f): if expression is set by the standing membrane,* $E = \iota\lambda\Lambda/\Lambda_0$*, instead of by the tethering event, the lineage does not settle. From the* 100*-nm founder the bud falls from* 47.15 *nm in generation 1 to* 16.72 *nm in generation 40,* 4.62 *nm in generation 80 and* 0.63 *nm in generation 150; from a* 30*-nm founder it reaches* 0.57 *nm by generation 150. A variant in which each site keeps excising, so that input scales with its area, enlarges monotonically over thirty generations instead (block X8(e)).*

Scholium 7.13 (Event and stock)**.** Both failures have one cause: an input that scales with the vessel's own extent. The tethering event is a flux and the tethered membrane is a stock. A flux set by the genome gives the set point; in the two computations a stock set by the vessel removes it, toward collapse or toward enlargement according to which way the stock scales against the lipid supply.

8 The population, and convergence

The set point of Proposition 7.9 is that of a mother line: at each division the computation follows the mother. Every division also makes a bud, which starts a line of its own. Both daughters inherit the free remnant per lipid w, since the reset splits membrane species by area, and differ in their lipids. This section treats the two extreme lines, the population between them, and the convergence of each.

Convention 8.1 (Scaled radius)**.** [D] At $c = 0$, with the catalyst at x^* (Proposition 7.3), the slice $w = \iota_{\text{eff}}$ is invariant: with $w_b = \iota_{\text{eff}}$, $W_b = \iota_{\text{eff}}\Lambda$ for the whole generation, and the reset preserves w. On it, write $\rho = R/k_R$ with $k_R = R_0\iota_{\text{eff}}/u_0$. A cell born at ρ_b has

$$v(\rho) = \frac{\rho_b^3 - \rho_b^2 + \rho^2}{\rho^3},$$

which involves neither ι_{eff} nor λ: in scaled radius the generation map depends on α alone. Write $\sigma = s_A^{1/2}$ and $\varsigma = b_A^{1/2}$.

Proposition 8.2 (The two extreme lines)**.** [D] *Under Hypotheses 2.6 and 2.12, at* $c = 0$*, on the slice, the mother line has a unique fixed point with bud born at* $\rho = 1$*, which is* $R_{\text{bud}} = R_0\iota_{\text{eff}}/u_0$*; the bud line, in which every division is followed into the bud, has a unique fixed point with bud born at*

$$\rho = \left(\frac{\alpha}{1-\alpha}\right)^{1/3},$$

0.4807 *at* $\alpha = 0.10$*. Computed at the baseline with* $c = 0.05$*: mother-line bud* 23.147 *nm, bud-line bud* 11.68 *nm. Block X10.*

Proof. A line with share $\theta_s \in \{s_A, b_A\}$ is stationary when $\rho_b = \theta_s^{1/2}\rho_d$ and $v(\rho_d) = v_{\text{thr}}(\alpha)$. Substituting, $\rho_d(v_{\text{thr}}(\alpha) - \theta_s^{3/2}) = 1 - \theta_s$. With $v_{\text{thr}}(\alpha) = Q(\alpha)^{-3/2}$, $s_A^{3/2} = (1-\alpha)Q(\alpha)^{-3/2}$ and $b_A^{3/2} = \alpha Q(\alpha)^{-3/2}$: for the mother $\rho_d = \alpha^{-1/3}Q(\alpha)^{1/2}$ and the bud is born at $\varsigma\rho_d = 1$; for the bud line $\rho_d = (1-\alpha)^{-1/3}Q(\alpha)^{1/2}$ and the bud is born at $\varsigma\rho_d = (\alpha/(1-\alpha))^{1/3}$. □

Theorem 8.3 (Every mother line converges)**.** *Under Hypotheses 2.6, 2.10 and 2.12, let $c = 0$ and $0 < \alpha < 1/2$, and consider the invariant set $\{x = x^*,\ w = \iota_{\text{eff}}\}$. Every mother line converges to the fixed point of Proposition 8.2, monotonically from its second generation.*

Proof. Division. $v(\rho_b) = 1$ and $v'(\rho) = -(\rho^2 + 3C)/\rho^4$ with $C = \rho_b^3 - \rho_b^2$, so v rises at most once and then falls to zero; it meets $v_{\text{thr}}(\alpha) < 1$ exactly once after ρ_b, at the root ρ_d of $h(\rho) = v_{\text{thr}}(\alpha)\rho^3 - \rho^2 - C$, where v is falling. The maximum of v is at least $v(\rho_b) = 1 > v_{\text{thr}}(\alpha)$, so the crossing lies strictly past it: $v' < 0$ there, hence $h'(\rho_d) > 0$ and $\rho_d > 2/(3v_{\text{thr}}(\alpha))$, and the root is a smooth function of C, so F is continuous.
Entry. The next birth is $F(\rho_b) = \sigma\rho_d > \frac{2}{3}\sigma/v_{\text{thr}}(\alpha) = \frac{2}{3}(1-\alpha)^{1/3}Q(\alpha)$, and $(1-\alpha)^{1/3}Q(\alpha) - 1 = \alpha^{2/3}\left[(1-\alpha)^{1/3} - \alpha^{1/3}\right] > 0$ for $\alpha < 1/2$. Every orbit is in $[2/3, \infty)$ after one step.
Monotonicity. On $[2/3, \infty)$, $dC/d\rho_b = \rho_b(3\rho_b - 2) \geq 0$, and the root of h rises with C because $h' > 0$ there; F is nondecreasing.
Sign. The fixed point is unique (Proposition 8.2). $F(2/3) > 2/3$ by the entry bound; for large ρ_b, $\rho_d \sim v_{\text{thr}}(\alpha)^{-1/3}\rho_b$ and $F(\rho_b) \sim (1-\alpha)^{1/3}\rho_b < \rho_b$. So $F(\rho) > \rho$ below the fixed point and $F(\rho) < \rho$ above it, and a nondecreasing self-map of $[2/3, \infty)$ with these signs carries every orbit monotonically to the fixed point. □

Proposition 8.4 (What is local and what is off the slice)**.** *(i) At $c = 0$ off the slice, $w_d - \iota_{\text{eff}} = (w_b - \iota_{\text{eff}})\Lambda_b/\Lambda_d$: the deviation contracts by the lipid ratio across each generation, $s_A = 0.8123$ on the mother line at $\alpha = 0.10$. (ii) Computed: the bud-line fixed point at $c = 0$ lies below $2/3$, where the map decreases, with slope -0.1480 at $\alpha = 0.10$; the global bound of Theorem 8.3 does not hold for the bud map when $\alpha < 1/2$. (iii) Computed, at the baseline with $c = 0.05$: the two-dimensional generation map on $(\ln\Lambda_b, w_b)$ has eigenvalues 0.9427 and 0.8017 at the mother-line fixed point and 0.1852 and -0.1487 at the bud-line fixed point. Both are locally stable. Block X11.*

Proposition 8.5 (The population)**.** *Computed at the baseline, from one cell at the mother-line fixed point (block X10). Followed genealogically to depth 12 (4096 cells), the birth radii run from 11.26 to 48.15 nm with median 23.43 nm. Followed in time to 20,000 births, keeping the second half, they run from 11.26 to 40.02 nm with median 23.43 nm. In both, 0.750 of births fall below $R_{\min} = 25$ nm.*
The fraction is structural, not sampled. At depth 12 every bud lies below the floor: the buds of buds at 11.26–12.53 nm and the buds of mothers at 12.62–23.15 nm. So do 1023 of the 1024 mothers whose parent was born a bud (23.43–26.06 nm). Every mother whose parent was born a mother lies above it (26.24–48.15 nm). The fraction is $\frac{1}{2} + \frac{1}{4}$ less one birth in 4096, and it is unchanged at 40,000 births.

Corollary 8.6 (Population viability)**.** *At $c = 0$ the birth-radius distribution in units of k_R depends on α alone, so viability of a fraction of births is a threshold on ι_{eff}. Computed over the time-weighted population (block X10):*

α	$\rho_{\min}$	*all births*	90%	50%
0.10	*0.4638*	*0.3513*	*0.3437*	*0.1689*
0.05	*0.3444*	*0.4732*	*0.4429*	*0.1765*
0.02	*0.2525*	*0.6452*	*0.6035*	*0.1763*

The columns give the least ι_{eff}. At $\alpha = 0.10$ a population in which every birth is viable needs $\iota_{\text{eff}} \geq 0.3513$, about twice the mother-line threshold 0.1629 of Proposition 7.6. The minimum radius $\rho_{\min}$ lies a little below the bud-line value of Proposition 8.2: mixed lineages reach lower than either pure line.

Scholium 8.7 (What a set point is here)**.** A budding lineage has no single size. It has a largest bud, made on the mother line and gauged by Theorem 7.4, and a distribution of smaller ones beneath it, reaching about $(\alpha/(1-\alpha))^{1/3}$ of the largest. What the genome specifies is the scale k_R of that distribution; its shape is fixed by α. Viability is a property of the distribution, and the mother line's bud is its most favourable member, not its typical one.

9 The gate as a tolerance

Proposition 7.12 compared two pure gates. A physical gate may mix them: expression triggered by tethering events, with a basal share proportional to the tethered membrane.

Definition 9.1 (The mixed gate)**.** $E = \eta\lambda\left[(1-\theta) + \theta\Lambda/\Lambda_{\text{ref}}\right]$, Λ_{ref} the mother's lipids at division on the $\theta = 0$ set point, so that θ is the basal share at division there.

Proposition 9.2 (Without condensation)**.** *Computed at $c = 0$, catalyst not limiting, $\iota_{\text{eff}} = 0.16$, $\alpha = 0.10$, $\Lambda_{\text{ref}} = 124{,}131$ lipids (block X12):*

θ	R_{bud} *(nm)*	τ	*slope*	*escape R (nm)*
0.00	*24.550*	*3.531*	*0.9483*	*> 2000*
0.10	*24.269*	*3.450*	*0.9574*	*513.1*
0.20	*23.833*	*3.328*	*0.9662*	*232.2*
0.30	*23.087*	*3.123*	*0.9744*	*139.8*
0.50	*18.792*	*2.069*	*0.9838*	*73.6*
0.70	*9.894*	*0.574*	*0.9744*	*59.9*

At every share tabulated the mother-line fixed point is locally stable; the basal share bounds its basin. A founder counts as escaping when its line has not converged within 1500 *generations or its lipid count exceeds* 10^9*; divergence is computed, not proved. The corpus founder of* 100 *nm escapes at* $\theta = 0.5$.

Proposition 9.3 (With condensation)**.** 🄳 *Computed at the baseline,* $c = 0.05$*, catalyst dynamic,* $\Lambda_{\text{ref}} = 110{,}348$ *lipids taken from the computed* $\theta = 0$ *fixed point, founders of* 30 *and* 300 *nm, bud radius at generation* 1200 *(block X12):* 23.147 *at* $\theta = 0$*,* 22.969 *at* 0.10*,* 22.568 *at* 0.25*,* 20.772 *at* 0.50 *and* 10.307 *at* 0.75*, the same from both founders. At* $\theta = 0.75$ *the two founders still differ at generation* 300 *(*10.323 *and* 16.095 *nm); the approach is slow, not absent.*

Scholium 9.4 (The gate hypothesis, weakened)**.** Hypothesis 2.8 asked for a pure event gate. What the loop needs is weaker: an event-triggered component, with the basal share below a tolerance that depends on how far founders lie from the set point. Under a pure stock gate neither normalization computed keeps a set point: normalized to the founder's membrane the lineage collapses (Proposition 7.12); normalized to the set point's, large founders run away. That no normalization keeps one is not proved (Target 12.7). The two tables of this section use different reference membranes and different treatments of the catalyst, so a given θ is not the same share in both, and the comparison between them is qualitative. And condensation, which Section 11 shows does not relieve the bilayer, earns a regulatory office here: it widens the basin, so that founders that escape without it are captured with it.

10 What the genome sets

Corollary 10.1 (Two genomic actions, two settings)**.** 🄳 *Under Definition 7.1:*

(i) the sequence content *sets the size, through* $\iota = \eta\Phi_G$ *(the class composition of the codons and their acceptance) and through* π' *(the fraction of* `AAA` *and* `TTT` *hexamers), which together fix* ι_{eff} *and the ceiling* $R_0\iota_{\text{eff}}/u_0$*;*

(ii) the genome length *sets the lipid flux* $\lambda = \nu L/2$ *and with it the period* $\tau = \Lambda_{\text{bud}}/\lambda$*, and, when* $c > 0$*, moves the bud toward its ceiling.*

Proof. (i) is Propositions 7.3 and 7.6 with Definition 6.6; L cancels from ι and π'. (ii) is Theorem 7.5, and the dependence of R_{bud} on L is Proposition 10.2. □

Proposition 10.2 (Genome length)**.** 🄳 *Computed, block X9(d), all three fluxes proportional to L:*

L	τ *(cycles)*	R_{bud} *(nm)*	w_{div}
200	*3.139*	*23.15*	*0.1509*
400	*1.658*	*23.79*	*0.1550*
800	*0.854*	*24.15*	*0.1574*
1000	*0.688*	*24.23*	*0.1579*
1200	*0.576*	*24.28*	*0.1582*

The period passes through one cycle between $L = 400$ *and* $L = 800$*.*

Proposition 10.3 (The forcing period with a viable bud)**.** 🄳 *By Theorem 7.5,* $\tau = 1$ *with* $R_{\text{bud}} \geq R_{\text{min}}$ *requires one cycle's lipids to close a vesicle of at least* 25 *nm:* $\nu L \geq 48{,}332$*, that is* $L \geq 732$ *at* $\nu = 66$*, or* $\nu \geq 242$ *at* $L = 200$*, beyond the range* 22–219 *that Article 62 sweeps. Block X6.*

Scholium 10.4 (The first specified phenotype)**.** Article 69 proposed that the genome would set the amplitude of the loop and not its period. The loop here gives a different and stronger reading. The genome sets both: the content of its codons sets how large a bud is, and its length sets how often one is made. Article 69's period identity survives as the special case in which the genome is just long enough for one cycle's lipids to close one bud.

Two qualifications go with the reading. The phenotype is specified, not regulated: the set point is fixed by the strand and responds to nothing. And the specification is not a code: classes are accepted at rates, no residue is assigned to a class, and Article 45's refutation of the correspondence with the standard code is untouched.

10.1 Bounds on the parameters

Assigning values to η, $a(\cdot)$, π, K and c without a source would present stipulation as data. Three things can be done without one: bound η by stoichiometry, reduce the acceptance table by a structure the corpus already has, and count what a genome supplies.

Hypothesis 10.5 (One codon per event)**.** [D] A lipid-tethering event triggers the expression of at most one codon: $\eta \le 1$. Registered as H10.

Proposition 10.6 (The sequence bound)**.** [D] *Under Hypothesis 10.5,* $\iota_{\text{eff}} \le \iota \le \Phi_G \le 1$. *A viable mother-line bud needs* $\Phi_G\, x^*/(x^* + K) \ge 0.1629$*, and at* $c = 0$ *a population with every birth viable needs it* ≥ 0.3513 *at* $\alpha = 0.10$ *(Corollary 8.6): the viability conditions become conditions on the sequence content.*

Definition 10.7 (Acceptance by stabiliser type)**.** [A] Article 45, Proposition 3.6, divides the twenty classes into four of stabiliser type r, four of type fr and twelve with trivial stabiliser. An acceptance table depending only on the type has three entries (a_r, a_{fr}, a_1) in place of twenty, and $\Phi_G = a_r \mu_G(\text{r}) + a_{fr}\mu_G(\text{fr}) + a_1 \mu_G(1)$. Under Hypothesis 2.13 the type-r classes are `00000` (`AAA`, `TTT`), `01010` (`ATA`, `TAT`), `10001` (`CAG`, `GTC`) and `11011` (`CTG`, `GAC`). Block X13.

Remark 10.8 (Why the type)**.** [E] The stabiliser type is the coarsest frame-invariant property of a class that the corpus has proved canonical, and the templating class `00000` is itself of type r. A tether that is itself a type-r hexamer accepting codons of its own type is a reading, used below as one illustration among the tables the definition admits.

Proposition 10.9 (What a genome supplies)**.** [D] *Computed for genomes of* 200 *units (*66 *codons) with independent letters, under the illustrative table* $a_r = 1$, $a_{fr} = a_1 = 0$, $\eta = 1$, *catalyst not limiting (block X13):*

	uniform	*A/T-rich*
μ_G(`00000`)	*0.0312*	*0.1280*
expected templates	*2.06*	*8.45*
P(no template)	*0.1230*	*0.0001*
mean Φ_G	*0.1250*	*0.2720*
sd Φ_G	*0.0407*	*0.0548*
P(necessary condition)	*0.1969*	*0.9843*

The A/T-rich genome draws `A` *and* `T` *at* 0.4 *each. The last row is the probability that at least* 11 *of the* 66 *codons are accepted, which is the necessary condition* $\Phi_G \ge 0.1629$ *for a viable mother-line bud at* $c = 0$ *with the catalyst not limiting. It bounds the probability of viability from above: for* $c > 0$ *the bud lies below its ceiling (Proposition 7.6), and at the baseline the catalyst lowers the input from* $\iota = 0.2$ *to* $\iota_{\text{eff}} = 0.1600$.

Proposition 10.10 (The catalyst supply)**.** [D] *Under Hypotheses 2.7 and 2.10, the supply condition* $3\pi' > \iota_{\text{eff}}$ *of Proposition 7.3, with* $\pi' = 2\pi\mu_G(\text{`00000`})/(3\nu)$*, requires* $\pi > \nu\iota_{\text{eff}}/(2\mu_G(\text{`00000`}))$ *triplets per template per cycle:* 169.0 *for a uniform genome and* 41.2 *for the A/T-rich one at* $\iota_{\text{eff}} = 0.16$, $\nu = 66$. *Block X13.*

Scholium 10.11 (What the sequence must be)**.** Under these bounds a random genome is unlikely to express the phenotype at all: one in eight carries no template, and its mean accepted fraction under the type-r table falls short of the mother-line threshold. An enriched genome does better on both counts, since the templating class and the accepted classes share members. The phenotype is therefore not generic to the architecture; it is a property of particular sequences, which is what a genetically specified phenotype should be.

11 What condensation does

Proposition 11.1 (A set point without condensation)**.** [D] *At* $c = 0$ *the loop still has a set point:* $w \to \iota_{\text{eff}}$ *and* $R_{\text{bud}} = R_0\iota_{\text{eff}}/u_0$*, the ceiling itself,* 24.55 *nm at the baseline with period* 3.531 *cycles (block X9(b)). In the single-use variant at* $\iota = 0.2$ *the bud at* $c = 0$ *is* 30.69 *nm, its ceiling* 30.7 *nm (block X8(a)).*

Proposition 11.2 (Condensation adds to the burden)**.** [D] *Each excision puts one remnant in the bilayer. Each condensation moves one remnant from free to sequestered and adds one residue to the co-aggregate. If the co-aggregate stays in the bilayer, condensation lowers the free remnant and the osmolyte and raises the total burden: from* 0.240 *per lipid at* $c = 0$ *to* 0.297 *at* $c = 1$ *at the baseline (Proposition 7.9). In the comparison design of block X7, where the burden has the closed form* $\iota(1 + 2\gamma_c)/(1 + \gamma_c)$*, it rises from* ι *toward* 2ι.

Remark 11.3 (The area the guests occupy)**.** [E] The burden of Proposition 11.2 consists of chrysene-sized units, with footprints of 0.39–0.43 nm^2 (Article 62, Corollary 7.7), against an area of $a/2$ per lipid in the bilayer. The loop counts only lipid area in A. Counting the guests would enlarge the area at a given lipid count, lower ν and bring division earlier, shifting the bud size and the period by an amount not computed here (Target 12.13).

Scholium 11.4 (The function of the first polypeptide)**.** Article 68 gave the polypeptide one office, to discharge the remnant at the rate it is made. Once lipids arrive as a flux, membrane growth bounds the remnant on its own: Article 67's ceiling does not arise (block X7(f)). What condensation does is osmotic. It removes residue from the lumen in proportion to the remnant it senses, which lowers the bud below its ceiling (Theorem 7.4, Proposition 7.6) and makes its size depend on the genome length (Proposition 10.2). The polypeptide sets the size of the next vessel, and under a mixed gate it widens the basin of the set point (Scholium 9.4). Whether it also relieves the bilayer depends wholly on the fate of the co-aggregate, which is Target 12.10.

Remark 11.5 (Two comparison designs)**.** [A] Blocks X6–X7 compute a design in which the genome's codons are themselves the condensation sites and the residue input is a fixed flux. There the free remnant converges exactly to $\iota/(1+\gamma_c)$ and Theorems 7.4 and 7.5 hold in the same form; splitting the remnant by α instead of by area moves the period at $\gamma_c = 10$ from 20.515 to 5.966 cycles. Block X8 computes the single-use triplet design of Proposition 7.11. Both are retained as comparisons and enter no statement about the loop.

12 Registers, precedence, targets, conclusion

12.1 Consolidated register

Is the fixed line of Article 69 reached by a dividing vessel?
No. One-cycle division requires no net growth, and a lineage held on the line reaches the dilution floor in 39.5 generations at $\alpha = 0.10$.
Rests on: Lem. 4.1, Cor. 4.4; blocks X1b, X1d.
Standing: [A] for the lemma; computed for the founder orbit.

What does the earlier system converge to?
A size-stationary line with $W_b = N$ at division, period $\tau(\alpha)$ (1.5102 cycles at $\alpha = 0.10$) or 2 in the per-cycle reading, size set by k.
Rests on: Prop. 4.2, Thm. 4.3; blocks X1c–X1e.
Standing: [D] ; convergence computed.

Can fixed membrane sites set a size under the input βN?
No: concave flux gives a neutral or unstable size; the genome sets a drift.
Rests on: Thm. 5.2, Cor. 5.3; blocks X2–X4.
Standing: [D] .

What is L_{lip}?
A per-cycle supply of 6,600 lipids, not the founder's membrane.
Rests on: Prop. 6.1; block P1l.
Standing: [D] : an inference from Article 67's transcription.

Which codons template the triplet?
`AAA` and `TTT`, the class `00000`.
Rests on: Prop. 6.4; block X5.
Standing: [D] on H9.

What gauges the bud?
The mother's free remnant per lipid at division: $R_{\mathrm{bud}} = R_0 w_{\mathrm{div}}/u_0$.
Rests on: Thm. 7.4.
Standing: [A] given size stationarity.

What sets the period?
The time to regrow one bud's lipids; T exactly when one cycle's lipids close one bud.
Rests on: Thm. 7.5.
Standing: [A] given size stationarity.

Does the loop have a set point?
The mother line does, from every founder tried: bud 23.147 nm, period 3.1388 cycles at the baseline, below the dilution floor.
Rests on: Prop. 7.9, Rem. 7.10; block X9.
Standing: [D] ; computed.

Does every mother line converge?
Without condensation, yes, for $\alpha < 1/2$; with it, locally (largest eigenvalue 0.9427 at the baseline).
Rests on: Thm. 8.3, Prop. 8.4; block X11.
Standing: [A] for the theorem; computed for the rest.

What does the population look like?
Buds from about $(\alpha/(1-\alpha))^{1/3}$ of the mother line's up to it; at the baseline 0.750 of births fall below the floor; every birth viable needs $\iota_{\mathrm{eff}} \geq 0.3513$ at $\alpha = 0.10$.
Rests on: Props. 8.2, 8.5, Cor. 8.6; block X10.
Standing: [A] for the extreme lines; computed for the distribution.

How much stock can the gate carry?
Any share tabulated up to 0.7 keeps a locally stable set point without condensation, with an escape radius falling from 513.1 to 59.9 nm; with condensation both founders converge up to 0.75.
Rests on: Props. 9.2, 9.3; block X12.
Standing: [D] ; computed.

What must the sequence be?
Under one codon per event, accepted fraction above 0.1629 for the mother line; a random 200-unit genome meets that necessary condition with probability 0.1969, an A/T-rich one 0.9843, under the type-r table. Both are upper bounds on viability.
Rests on: Props. 10.6, 10.9; block X13.
Standing: [D] on H10; computed for the genomes.

What does the genome set?
Content sets size; length sets period.
Rests on: Cor. 10.1, Prop. 10.2.

Standing: [D] on H1–H9.

What does condensation do?
Sets the size below its ceiling; raises the bilayer burden unless the co-aggregate leaves.
Rests on: Props. 11.1, 11.2; Sch. 11.4.
Standing: [D] .

What does the set point turn on?
The gate being the tethering event; the stock gate collapses the lineage.
Rests on: Prop. 7.12; block X9(f).
Standing: [D] on H4; computed.

12.2 Falsification register

Lemma 4.1
A vessel born at $v = 1$ that divides after one cycle with net growth, which would require an area model other than growth by $Q(\alpha)$ per cycle.

Theorem 7.4
A loop with $\dot{N} = \dot{W}_b$, membrane species split by area and a size-stationary mother line whose bud is not born at w_{div} osmolyte per lipid. The statement fails if residue and remnant are not made together, one each per excision.

Theorem 7.5
A stationary period other than $\Lambda_{\mathrm{bud}}/\lambda$: a lipid supply that is not constant per cycle, or a membrane species split other than by area.

Proposition 7.3
A catalyst whose consumption is not one unit per excision, or whose supply is not three units per triplet.

Hypothesis 2.8, Proposition 7.12
Codon expression proportional to the tethered membrane rather than to tethering events. This is the most expensive refutation: the set point is lost.

Hypothesis 2.7, Proposition 6.4
A triplet complex templated by codons outside `00000`, or not integrated in the bilayer as the patent figures show.

Proposition 11.2
A co-aggregate expelled from the bilayer as fast as it forms, which would refute the burden statement in the favourable direction.

Theorem 8.3
A mother line at $c = 0$ and $\alpha < 1/2$ on the slice that fails to converge; the proof would then have an error, since the statement uses only the threshold, the area-split reset and linear supplies.

Corollary 8.6
A population at $\iota_{\mathrm{eff}} \geq 0.3513$ and $\alpha = 0.10$, $c = 0$, with a birth below the floor.

Hypothesis 10.5
A tethering event that triggers more than one codon, which would loosen every bound of Section 10.1.

Proposition 6.1
An allocation in Article 65 whose lipid entry is a standing count of the founder's membrane.

12.3 Precedence

The rulings record corrections to earlier articles in the order of their weight here. Corrected statements supersede the earlier ones where they speak to the same object; the earlier text is not altered. Table 2 collects the corrected values.

Ruling 12.1 (Against Article 69)**. 69.1** [A] *Theorem (period) is restated.* It is correct of a vessel born on the fixed line, and no dividing vessel is born there (Corollary 4.4). Its status is [D] , the line existing only under the linear model. The identity $v_{\mathrm{thr}}(\alpha) \cdot Q(\alpha)^{3/2} = 1$ restates Article 64's area model, one division's membrane per cycle; "not a design choice" in Scholium (self-tuning) and block V3 is withdrawn. Its new form is Theorem 7.5.

69.2 [A] *Corollary (closure)(iii) is reversed.* A lineage dividing every T has no net growth and reaches the dilution floor in 39.5 generations at $\alpha = 0.10$ (Lemma 4.1): Article 64's forty-generation bound applies on the fixed line. The first sentence of Ruling (Against Article 64) of Article 69 is withdrawn; its import of the area model stands.

69.3 [D] *Remark (transient period) is corrected.* The period does not converge from two cycles to one; it is $\tau(\alpha)$ in the continuous reading and 2 in the per-cycle reading (Theorem 4.3). The post-division factor at $\alpha = 0.10$ is 0.8947 for the bud and 0.8224 for the mother, both with $k_{\mathrm{div}} = 2$; the printed 0.914 was emitted by no block. Block P1d.

69.4 [D] *Corollary (closure)(i)–(ii) are restated.* In the earlier system the remnant is bounded because N tracks W_b (Proposition 4.2), not because W_b rests at W_b^*. In the loop of this article it is bounded by membrane growth (Scholium 11.4).

69.5 [A] *Stability claims are narrowed.* Theorem (stable) is local and "globally attracting" is withdrawn. Proposition (global) holds for $k < 2L_{\mathrm{lip}}/N_{\mathrm{max}} = 0.0764$ ($N_{\mathrm{max}} = 1.372\,N_0$), not for all k in the safe range; Proposition (regimes) holds on the monotone subrange only. The eigenvalue table is replaced by block P1e.

69.6 [A] *The falsification entry for Corollary (closure)(ii) is replaced.* The k-interval of Article 68 is non-empty

only if $\varrho_{\max} > \beta N_0/(2L_{\text{lip}})$: 1.061, 0.502, 0.195 at $\alpha = 0.10, 0.05, 0.02$. Block P1f.

69.7 [A] *Definition (map) reset* is corrected to Convention 2.2. Block X1a.

69.8 [D] *Target (encoder) is closed in a changed form.* The genome sets the size of the bud and the period, not the amplitude alone (Corollary 10.1). On the input of Article 67, with condensation limited by the genome's membrane sites and linear or saturating in the remnant, it sets only a drift (Theorem 5.2); Article 69's linear model sets a size through k only because it makes the flux proportional to the particle count (Theorem 4.3).

Ruling 12.2 (Against Article 68)**. 68.1** [A] *The direction of the transient is corrected.* Block W4 and the governor remark state that $f_c < \beta$ makes division sooner. It makes it later, N growing and v falling more slowly. At $\alpha = 0.10$, $k_{\text{div}} = 3, 2, 1, 1$ for $f_c/\beta = 0, 0.5, 1, 1.5$. Block P1k.

68.2 [E] *"Discharge" is restated as sequestration in place.* The co-aggregate stays in the bilayer: on the fixed line the bilayer receives βN_0 residues per cycle, $2.12\,L_{\text{lip}}$ at $\alpha = 0.10$, with as many sequestered remnants (block P1g). The office of the polypeptide is restated in Scholium 11.4.

68.3 [E] *The stacking estimate is withdrawn as a sequestration fraction.* $\exp(E_{\text{stack}}/k_B T)$ is not an association constant and 82–97% refers to no concentration; read as K_a in M^{-1} the bound fraction at equimolar 1 mM is 0.5–2.7% and at 1 M 63–83% (block P1i). One-to-one sequestration is Hypothesis 2.12.

68.4 [A] *Block W2.* Aromatic hydrocarbons have positive $\log P$; the transfer free energy is -19.5 to $-35.0\ \text{kJ mol}^{-1}$ per aromatic fragment, not per chain. Block P1h.

68.5 [A] *The hexameric-site geometry is suspended.* The ring of side 14 Å, free diameter 9.17 Å and clearance 3.77 Å is cited, under the key for Article 24, to the third loom paper [Sch26b], which this article has not consulted. The article published as Article 24 [Sch26a] contains none of the three figures. The 5.4 Å of Article 23, Theorem 6 [Sch26d], is a helical pitch, so if the clearance is 9.17−5.4 it subtracts a pitch from a diameter (block P1j). The clearance is suspended pending a check against the third loom paper; the site is in any case replaced here (Ruling 68.7).

68.6 [A] *Block W1.* 10–20 kJ mol^{-1} is a reaction free energy for amide formation, not an activation energy.

68.7 [D] *Hypothesis H1 and the site are replaced.* The linear model gives way to Hypothesis 2.11, and the condensation site is the `X-A` catalyst of Hypothesis 2.7 (U.S. Patent 12,195,423, Figures 15A–C and 20) in place of the hexameric ring.

Ruling 12.3 (Against Article 67)**. 67.1** [A] *Definition (reset)* is corrected to Convention 2.2: as printed the bud has $v = v_{\text{thr}}(\alpha)$ and the daughter areas sum to $Q(\alpha)A$. Block X1a.

67.2 [A] *Crossover values.* At $\varrho_{\max} = 5$, $\alpha_c = 0.0065$ for $K_{\text{safe}} = 40$ and 0.0255 for $K_{\text{safe}} = 10$; the printed 0.013 and 0.031 are not emitted, 0.013 being the entry at $\varrho_{\max} = 10$. Block P1a.

67.3 [A] *Remark (clock).* $f(0.20) = 0.9464 < 1$; clock-forced division begins at $\alpha = 0.2640$. Block P1b.

67.4 [A] *Photon energies* are 341.8 and 299.1 kJ mol^{-1} at 350 and 400 nm; block V5 carried a factor 2π. Both exceed E_{T_1}; the conclusion stands. Block P1c.

67.5 [E] *"Five to ten events per photon" is withdrawn.* 4.8 and 9.5 are energy ratios; one triplet excitation drives at most one event, so the demand of 0.648 s^{-1} per vessel at $\alpha = 0.10$ is also the minimum absorbed-photon rate. "Easily satisfiable" contradicts Non-implication (v) and is withdrawn. Block P1c.

67.6 [A] *Terminology.* $\varrho = R/N$ is not an invariant of the per-cycle map; the form of its update is, and $R - N$ is (Proposition 4.2).

67.7 [A] L_{lip} *is a per-cycle supply* (Proposition 6.1). Read as the founder's standing count it is short by 58.6; every load W_b/L_{lip} of Articles 67–69 inherits the factor. Blocks P1l, P1m.

67.8 [A] *Block file.* Blocks V2–V3 print working notes, a reading contradicted by the table beneath it, and negative return times at $\alpha \geq 0.30$; the file is to be regenerated. No number here depends on it.

Ruling 12.4 (Against Article 64)**.** [A] Consistent. The area-conserving reset of Lemma (taut) is the one used here (Convention 2.2). The forty-generation bound stands wherever the lineage has no net growth, including the fixed line of Article 69.

Ruling 12.5 (Against Article 62)**.** [A] Consistent; one use added. The closure ratio ν is read as the per-cycle lipid flux of one strand, and the closure radius acquires a dynamical meaning: the period equals T exactly when the bud is the vesicle that one cycle's lipids close (Theorem 7.5). The anchoring of the strand to the inner leaflet is Hypothesis 2.5.

Ruling 12.6 (Against Article 45)**.** [A] Consistent; one instance added. The functional of Definition 6.6 is instantiated with the genome's codon classes as ensemble and the acceptance table as weight (Remark 6.7). Targets 7.5 and 7.6 are touched and not discharged; Proposition 3.15 is untouched.

12.4 Targets

Target 12.7 (The gate)**.** Determine the basal share θ of codon expression that is proportional to the tethered membrane. A pure stock gate lost the set point in both normalizations computed (Proposition 7.12), and whether any normalization keeps one is open; a mixed gate keeps the set point within a basin bounded by θ (Section 9). The share is to be settled against the synthesis-phase tethering of U.S. Patent 12,195,423.

Target 12.8 (The constants)**.** Supply $\eta \le 1$, the three entries (a_r, a_{fr}, a_1) of the type table or a sourced table on the twenty classes, π (bounded below by Proposition 10.10), K and c. Until then the figures illustrate identities and predict nothing.

Target 12.9 (Viability)**.** Determine whether $\iota_{\text{eff}} \ge 0.1629$ is met, so that the mother line's bud clears the floor (Proposition 7.6), whether the population threshold of Corollary 8.6 is met, and whether $\nu L \ge 48{,}332$ is met, so that the period is T with a viable bud (Proposition 10.3).

Target 12.10 (The fate of the co-aggregate)**.** Determine whether the co-aggregate of condensed residue and sequestered remnant leaves the bilayer. The burden of Proposition 11.2 turns on it, and with it whether condensation relieves the membrane at all. Inherits Article 69, Target (fate).

Target 12.11 (Global convergence)**.** Extend Theorem 8.3 off the slice, to the bud line, to $\alpha \ge 1/2$ and to $c > 0$, where only local stability is computed (Proposition 8.4); and determine the stationary birth-size distribution of the population analytically.

Target 12.12 (The reading frame)**.** Codons are read in non-overlapping triplets from the first unit (Definition 6.3). Decide whether the frame is fixed by the strand, and what the other two frames would contribute to μ_G.

Target 12.13 (The guest area)**.** Count the membrane area occupied by catalyst, remnant and co-aggregate in the area that enters ν, and recompute the set point, the population and the period (Remark 11.3).

Target 12.14 (The founder's membrane)**.** Confirm against Articles 64 and 65 that the lipid entry is a per-cycle supply, and state how the 773,315 units of the founder's membrane were assembled before the first cycle.

12.5 Conclusion

Proposition 12.15 (What is established)**.** [A] *Subject to Appendix A:*

(i) With division included, the fixed line of Article 69 is not occupied, and a lineage held there meets the dilution floor; the earlier system divides in $\tau(\alpha)$ cycles at a size set by k (Lemma 4.1, Theorem 4.3).

(ii) Under an osmolyte input proportional to the particle count, a fixed number of membrane sites with a flux linear or saturating in the remnant cannot set a size; the genome sets a drift (Theorem 5.2).

(iii) The lipid entry of the allocation is a per-cycle supply (Proposition 6.1).

(iv) On the loop of Definition 7.1: the catalyst density is the root of a quadratic; the bud is gauged by the remnant, $R_{\text{bud}} = R_0 w_{\text{div}}/u_0$; the period is the time to make one bud's lipids, equal to T exactly when one cycle's lipids close one bud; and the free remnant is capped by ι_{eff} (Propositions 7.3, 7.6, Theorems 7.4, 7.5).

(v) Computed: a mother-line set point reached from every founder tried, below the dilution floor at the baseline; reuse of the unexcised units lowers the triplet demand and the burden; a gate on the stock alone loses the set point in both normalizations computed (Propositions 7.9–7.12).

(vi) The mother line's bud is the largest of a distribution reaching about $(\alpha/(1-\alpha))^{1/3}$ of it; without conden-

sation every mother line converges for $\alpha < 1/2$; population viability needs about twice the mother line's input (Proposition 8.2, Theorem 8.3, Corollary 8.6).

(vii) A mixed gate keeps the set point locally, with a basin that the basal share bounds and condensation widens (Propositions 9.2, 9.3).

(viii) Under one codon per event the viability conditions are conditions on the sequence content; random genomes rarely meet even the necessary condition and enriched ones usually do, under the type table (Propositions 10.6, 10.9).

(ix) The sequence content sets the size and the genome length sets the period (Corollary 10.1).

(x) Condensation sets the size and does not by itself relieve the bilayer (Propositions 11.1, 11.2).

Remark 12.16 (What is not established, restated)**.** 🄰 No parameter of the loop is known, so no size or period is predicted. The baseline bud lies below the dilution floor, and three births in four lie below it. Convergence is proved only without condensation and only for mother lines. The type table is an illustration, not a derivation. The acceptance of codons by class is not a code. And the set point rests on one premise, an event-triggered gate with a bounded basal share, that the patent record is asked to decide.

A Hypothesis register

Remark A.1 (The dependency, in one sentence)**.** 🄰 H4 carries the set point; H8 carries the gauge; H2 carries the period; H3, H5 and H6 carry figures; H9 carries a name; H10 carries the sequence bounds; and Sections 4–5 rest on none of them.

B Verification

Every number in the body is emitted by `acf-71-blocks.py` (standard library only; a full run takes the better part of an hour, the integrations of X8, X9 and X12 dominating).

X1 [COMPUTED] **The hybrid attractor**

The reset normalisation; one-cycle division and the generations to the floor; invariance of $W_b - N$ under three laws; the founder orbit and the attractor in both readings, with $\tau(\alpha)$ and u^* in closed form against event-driven simulation.

X2–X4 [COMPUTED] **Fixed sites under the input βN**

Cancellation of L; the slopes of the birth-size map for seven laws; the drift, the viable band and the founder transient.

X5 [COMPUTED] **The registry hexamer**

The sixty-four codons on the twenty classes, fibre sizes eight of two and twelve of four; `AAA` and `TTT` alone in `00000`.

X6–X7 [COMPUTED] **Comparison design**

Codons as sites with a fixed input; the exact free remnant, bud and period against simulation; the reset convention; the burden in closed form.

X8 [COMPUTED] **Single-use triplets**

The four identities; set point against c; founders; length; bud fraction; the area-scaled variant.

X9 [COMPUTED] **The loop**

Catalyst density against supply; set point against c; founders; genome length; reuse against X8; the two gates.

X10 [COMPUTED] **The population**

The two extreme lines in closed form against the generation map; the genealogical and time-weighted birth distributions, the decomposition of the below-floor fraction by lineage, and its stability at 40,000 births; the viability thresholds on ι_{eff}.

X11 [COMPUTED] **Convergence**

The entry bound and the slope at the mother-line fixed point; iterates from five starts; the bud line; the Jacobian at both line fixed points for $c > 0$.

X12 [COMPUTED] **The mixed gate**

Fixed point, slope and escape radius against θ without condensation, with the escape criterion stated; both founders at generations 300 and 1200 with condensation, the reference membrane taken from the computed fixed point.

X13 [COMPUTED] **Parameters**

The stoichiometric bound; the type table; templates and accepted fractions of uniform and A/T-rich genomes; the catalyst-supply bound.

P1 [COMPUTED] **Precedence audit**

Every number cited by the rulings: crossover values, clock onset, photon energies, transient factors, stability bounds, feasibility thresholds, influx, transfer energies, binding fractions, site provenance, the lipid count and the ceiling under both readings.

Representative output, block X9(c) and (f):

```
R_init =    30 nm:  tau = 3.1388   R_bud = 23.147 nm
R_init =   100 nm:  tau = 3.1388   R_bud = 23.147 nm
R_init =   300 nm:  tau = 3.1388   R_bud = 23.147 nm
area gate, gen   1:  tau =   10.796   R_bud =   47.15 nm
area gate, gen 150:  tau =    0.002   R_bud =    0.63 nm
```

Table 1: Hypotheses of this article: what rests on each, and what survives its failure.

	Premise	What rests on it	What survives its failure
H1	One strand, anchored (Hyp. 2.5)	The proportionality of all three fluxes to L	Sections 4–5; the identities of Thms. 7.4, 7.5
H2	Lipids at $\nu L/2$ per cycle (Hyp. 2.6)	The membrane as a state fed by a flux; Thm. 7.5	Prop. 6.1 as arithmetic; Sections 4–5
H3	Triplets from `00000`, in the bilayer (Hyp. 2.7; patent figures cited by the author, to be confirmed at the editorial stage)	The catalyst supply π'	Thm. 7.4 and Thm. 7.5, which need no catalyst
H4	Expression on the tethering event, basal share admitted (Hyp. 2.8; the tethering figure to be identified at the editorial stage)	The set point and its basin	The exact identities; with the stock alone the set point is lost in both computed normalizations (Prop. 7.12)
H5	Acceptance by class (Hyp. 2.9)	The reading of ι as $\eta\Phi_G$	The loop with ι a constant
H6	The site cycle (Hyp. 2.10)	Prop. 7.3; reuse	The single-use design of block X8
H7	Condensation at the catalyst (Hyp. 2.11)	The size below the ceiling; the dependence on L	The set point at $c = 0$ (Prop. 11.1)
H8	One-to-one sequestration (Hyp. 2.12)	$\dot{N} = \dot{W}_b$, hence Thm. 7.4	Thm. 7.5; the set point with a different gauge
H9	Base to letter (Hyp. 2.13)	Prop. 6.4, the class of the templates	Everything with n_A taken as given
H10	One codon per event (Hyp. 10.5)	The sequence bounds of Section 10.1	Everything else

C Correction ledger

D Revision record

The referee's required items and their dispositions, in the critique–revision–verification form of the review architecture. Every item was accepted. Item A1 was found by the author while assembling the sources of Appendix E, after the review.

The recommended items not taken up in this revision are the per-cycle reading of the loop, a version of Theorem 7.4 for $\varepsilon < 1$, a figure of the birth-radius distribution, and the analytic population distribution, which remains Target 12.11.

E Sources and literature

This appendix records where each source enters the article, so that the provenance of every imported statement can be checked without returning to the source. Corpus articles and the patent record carry the argument; the established literature of the third subsection below is context and enters no proof.

E.1 The corpus, by use

Table 4 lists the articles of the corpus on which this article draws, where each is used, and what is taken.

E.2 The patent record

Three things are taken from U.S. Patent 12,195,423 [Sch25a], whose figures also appear in the divisional U.S. Patent 12,473,247 [Sch25b].

(i) One lipid particle from one pair of substituted chrysenes (Hypothesis 2.6), the unrecruited dimer of Article 62 [Sch26f], Proposition 4.9, which cites the patent's Figure 16b.

(ii) The tethered adenosine–chrysene triplet `X-A X-A X-A` integrated in the phospholipid bilayer (Hypothesis 2.7), Figures 15A, 15B, 15C and 20, cited as the author supplies them and recorded for editorial confirmation in Appendix A.

(iii) The tethering of the membrane to the genome established in the synthesis phase (Hypothesis 2.8), with the figure to be identified at the editorial stage.

E.3 Established literature

None of the following enters a proof. Each is cited so that the machinery this article borrows, and the questions it shares with other fields, are visible in one place.

Vesicle shape. The reduced volume $v = V/V_{\mathrm{sph}}(A)$ that sets the division threshold of Article 64 is the standard shape parameter of fluid vesicles [Sei97].

Hybrid dynamics. The loops of Sections 4–9 flow between divisions and jump at a threshold; the framework of flow, jump set and reset map is that of hybrid dynamical systems [GST12]. Nothing beyond its vocabulary is used.

One-dimensional maps. The last step of Theorem 8.3, that a nondecreasing self-map of an interval with a single fixed point, above the diagonal below it and below the diagonal above it, carries every orbit monotonically to that point, is standard [Ela05].

Iterated function systems. At $c = 0$ the population of Section 8 is generated by two explicit maps, the mother step and the bud step, applied in every order: a two-map iterated function system [Hut81]. Its invariant measure is Target 12.11.

Table 2: Correction ledger for Articles 67–69. Every corrected value is emitted by `acf-71-blocks.py`.

Art.	Location	As printed	Corrected	Block
67	Def. reset; Art. 69 Def. map	$\alpha^{2/3}A$	$\alpha^{2/3}A/Q(\alpha)$	X1a
67	Intro.; Cor. crossover	$\alpha_c = 0.013, 0.031$	0.0065, 0.0255	P1a
67	Rem. clock	$f \geq 1$ at $\alpha \geq 0.20$	$f = 1$ at $\alpha = 0.2640$	P1b
67	Block V5	2147.5, 1879.1 kJ/mol	341.8, 299.1 kJ/mol	P1c
67	Intro.; Block V5	5–10 events/photon	quantum yield ≤ 1	P1c
67	L_{lip} read as standing count	13,200 units	per-cycle supply; founder 773,315	P1l
68	Block W4; governor remark	$f_c < \beta$: sooner	$f_c < \beta$: later	P1k
68	Block W2	$\log P$ negative; per chain	positive; per fragment	P1h
68	Prop. stacking	83–97% sequestered	concentration-dependent	P1i
66, 68, 69	Site geometry (cited under the key for Art. 24)	clearance 3.77 Å	suspended; 5.4 Å is a pitch	P1j
69	Thm. period; Cor. closure(iii)	period T, bound superseded	line not occupied; bound applies there	X1b, X1d
69	Rem. transient	period $2 \to 1$; $f_{\mathrm{tr}} = 0.914$	$\tau(\alpha)$ or 2; 0.8947/0.8224	X1e, P1d
69	Prop. global	all k in safe range	$k < 0.0764$	P1e
69	Falsification, Cor. closure(ii)	circular entry	$\varrho_{\max} > \beta N_0/(2L_{\mathrm{lip}})$	P1f

Cell-size control. The question this article puts to a budding lineage, what fixes the size at birth and whether a perturbed size is restored, is the question studied in bacterial size homeostasis, where sizer, timer and adder models are compared with single-cell data [Ami14, TABS+15]. Those models are not used, and no correspondence with them is asserted.

Protocell growth and division. Fatty-acid vesicles grow by incorporating amphiphile and divide under modest forces, and osmotic content couples to membrane growth [CRS04, ZS09]. The reduced-volume threshold of Article 64 is a model of that coupling. No quantitative correspondence is asserted.

E.4 Notes on the corpus's citations

Three discrepancies were found in assembling Table 4, and are recorded rather than reconciled.

(i) Articles 67 and 68 cite the third loom paper, *Higher-Order Geometry of the Abiotic Loom*, under the key for Article 24, while the article published as Article 24 is *Geometric Validation of the Abiotic Loom*. This article cites both by title. It is the source of item A1 of Appendix D.

(ii) Articles 67 and 68 place Article 62 in Volume 1, Number 3; Article 62's own header places it in Number 4 at page 1401, which is followed here.

(iii) Article 45 gives its pages as 676–704 in its citation line and its start page as 675 in its Remark B.3; the citation line is followed.

References

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[GST12] R. Goebel, R. G. Sanfelice, and A. R. Teel. *Hybrid Dynamical Systems: Modeling, Stability, and Robustness*. Princeton University Press, 2012.

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[Sch25a] Charles D. Schaper. Encoded Design Integrated Synthesis of Nucleic Acids, and Phospholipids, and Related Pharmaceutical Products. U.S. Patent No. 12,195,423, 2025. Figures 15A–C, 16b and 20.

[Sch25b] Charles D. Schaper. Encoded Design Integrated Synthesis of Nucleic Acids, and Phospholipids, and Related Pharmaceutical Products. U.S. Patent No. 12,473,247 B2, 2025. Divisional of U.S. Patent No. 12,195,423.

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[Sch26c] Charles D. Schaper. Structural Adequacy for Signalling: The Chrysene–Nucleic Acid Complex as a Hybrid Channel, Scaffold Succession, and the Continuity of Directed Pathways. *Annals of the Chrysene Formalism*, 1(3):1321–1347, 2026. Article 63. DOI: https://doi.org/10.68366/0e3gsg12.

[Sch26d] Charles D. Schaper. The Abiotic Loom: Discrete Morse Theory and the Geometric Resolution of Levinthal's Para-

Table 3: Response to the referee report.

Item	Critique	Revision and where verified
R1	Eight statements labelled A rest on registered hypotheses	Relabelled D with the hypotheses named: Props. 7.3, 7.6, 8.2, 10.6, 10.10; Thms. 7.4, 7.5, 8.3; Conv. 8.1
R2	Thm. 8.3 uses $x = x^*$ unnamed; proof gives only $h' \geq 0$	Stated on $\{x = x^*,\ w = \iota_{\text{eff}}\}$; strictness and continuity of F added to the proof
R3	Thm. 5.2 asserts existence it does not prove	Restated for a fixed point where one exists; existence named as not supplied
R4	Genome probabilities reported as viability	Renamed the necessary condition, stated as upper bounds: Prop. 10.9, abstract, register, conclusion; block X13 relabelled
R5	The 0.750 unexplained	Decomposition by lineage added to Prop. 8.5, emitted by block X10 with the 40,000-birth check
R6	Escape stated as divergence	Criterion stated; divergence marked computed, not proved: Prop. 9.2, block X12
R7	"No stable scale" from two instances	Restated as the two normalizations computed: Scholia 9.4, abstract, register, targets, conclusion
R8	Mixed-gate tables not comparable	Reference membrane of Prop. 9.3 taken from the computed fixed point; comparison marked qualitative in Sch. 9.4
R9	Prop. 6.1 an inference labelled arithmetic	Relabelled D ; the inference named in statement and proof
C1	(α, β) collides with α, β	Written $(\alpha_{62}, \beta_{62})$ in Hyp. 2.13
C2	Sections 4–5 inherit the misread L_{lip}	Rem. 5.5 separates what survives
C4	Periods carry the stipulation in ν	Rem. 7.8
D1	Patent figures not seen by the reviewer	Recorded in the hypothesis register for editorial confirmation
D2	Guest area not counted (recommended)	Named with its sign, Rem. 11.3; Target 12.13
D3	Residue route assumed (recommended)	Non-implication added, Prop. 3.1
A1	Author, after review: Ruling 68.5 judged the site geometry unsourced from the article published as Article 24, while Articles 67–68 cite it to the third loom paper	Restated as a source not consulted and a clearance suspended; Ruling 68.5, block P1j, Table 2, Appendix E

dox in the Chrysene Tensor Space. *Annals of the Chrysene Formalism*, 1(1):273–282, 2026. Article 23. DOI: https://doi.org/10.68366/vdze9508.

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[Sch26k] Charles D. Schaper. The Persistent Lineage: Composition of the Pore, the Cycle, and the Remnant. *Annals of the Chrysene Formalism*, 1(3):1405–1413, 2026. Article 67. DOI: https://doi.org/10.68366/h6d6b415.

[Sch26l] Charles D. Schaper. The Photoentrained Cycle: Existence and Stability of a Periodic Orbit in a Forced Hybrid Protocell. *Annals of the Chrysene Formalism*, 1(3):1348–1370, 2026. Article 64. DOI: https://doi.org/10.68366/h9rzkd75.

[Sch26m] Charles D. Schaper. The Twenty Registry Classes of a Chrysene Stack: Frame Orbits, Descent of a Letter Transformation, and a Variational Criterion. *Annals of the Chrysene Formalism*, 1(2):676–704, 2026. Article 45. DOI: https://doi.org/10.68366/vfjz1403.

Table 4: Corpus sources by use.

Source	Used at	What is taken
Coordinating paper [Sch26j]	Conv. 2.1	The status labels A , D , C , E and the convention that scholia enter no proof.
The Abiotic Loom [Sch26d]	Ruling 68.5; block P1j	Theorem 6: the 5.4 Å spacing between successive helical turns.
Geometric Validation of the Abiotic Loom [Sch26a]	Ruling 68.5; block P1j	Read for the hexameric-site figures, which it does not contain.
Higher-Order Geometry of the Abiotic Loom [Sch26b]	Ruling 68.5	Cited by Articles 67–68 for the site geometry; not consulted here.
The Twenty Registry Classes [Sch26m]	Defs. 6.3, 6.6, 10.7; Props. 6.4, 10.9; Hyp. 2.13; Rem. 6.7; Ruling (Against Article 45)	The six-site stack and its frame group; the twenty classes and their fibre profile (Cor. 3.7); stabiliser types and the central entry (Prop. 3.6); the coordinates (b_1, b_2) (Def. 3.12); the functional Φ (Def. 6.6); the refutation of a correspondence with the genetic code (Prop. 3.15).
The Enclosure [Sch26f]	Hyps. 2.5, 2.6, 2.13; Prop. 6.1; Thm. 7.5; Rems. 7.8, 11.3; Ruling (Against Article 62)	The strand anchored to the inner leaflet (Sec. 8); the closure ratio ν and its range (Thm. 10.5, Cor. 10.6); one lipid to a pair of units (Prop. 10.2); $N(R) = 8\pi R^2/a$ with $a = 0.65$ nm^2 (Def. 10.1); the orientational datum (Def. 4.7); the footprint of a chrysene unit (Cor. 7.7).
Structural Adequacy for Signalling [Sch26c]	Rulings 67.4–67.5; block P1c	The triplet energy $E_{T_1} = 143$ kJ mol^{-1}.
The Photoentrained Cycle [Sch26l]	Conv. 2.2; Lemma 4.1; Ruling (Against Article 64)	The reduced volume and the threshold $v_{\mathrm{thr}}(\alpha) = Q(\alpha)^{-3/2}$; Lemma (taut); the area model; N_0, T, R_0, $R_{\min}$; the forty-generation bound.
The Material Ledger [Sch26e]	Prop. 6.1; Target 12.14	The allocation of a single pool, through Article 67's transcription; not consulted directly.
The First Pore [Sch26i]	Section 4; Ruling 68.5	The pore that supplies the osmolyte input of the earlier system; the site citation.
The Persistent Lineage [Sch26k]	Sections 4 and 5; Prop. 6.1; Ruling (Against Article 67)	The per-cycle map and reset; the excision edge; the allocation as transcribed in block V1; the remnant ceiling.
The First Polypeptide [Sch26h]	Sections 4 and 5; Hyps. 2.11, 2.12; Ruling (Against Article 68)	The condensation edge; the linear model H1, replaced here; one-to-one sequestration, named here.
The First Loop [Sch26g]	Sections 4 and 7; Rem. 7.7; Ruling (Against Article 69)	The fixed line; the remark on equal increments; the period identity; `tgt:encoder`, which this article takes as its mandate.

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