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Computational Verification Code: Article 64

The Photoentrained Cycle

Existence and Stability of a Periodic Orbit in a Forced Hybrid Protocell

Author: Charles D. Schaper, Ph.D. | **Artifact:** `verify_photoentrained_cycle.py` ⟶ console report (664 lines, 80 checks)

Verification Certificate & Reproducibility Protocol

Every arithmetic assertion of Article 64 — each characteristic time, barrier height, drag coefficient, return-map multiplier, division threshold, population exponent, genome cap, loop gain and printed table row — is recomputed by the standalone script `verify_photoentrained_cycle.py` listed in Section 4. The script imports nothing from the manuscript: the division geometry, the two return maps, the Saffman–Delbrück drag law, the three caps and the mechanochemical gain are rebuilt from their definitions, so that agreement is evidence rather than restatement.

- **Zero External Dependencies:** Python 3.8 or later, standard library only (`math`, `sys`); no third-party package and no numerical library, which secures long-term reproducibility.
- **Determinism:** No pseudorandom quantity enters any check. Every computation is a closed-form evaluation or a sweep over an explicit grid. Repeated runs on any platform produce identical output.
- **Execution Command:** Run `python3 verify_photoentrained_cycle.py` for the summary, or with the `-v` flag for the per-check transcript reproduced in Section 5. The process exits 0 if every check passes and 1 otherwise, so the script serves as a build-time gate.
- **Verification Status: PASSED** — 80 of 80 checks in Blocks `V1`–`V9`, the cross-block block `X` and the errata block `E`; exit code 0. Three figures of the published Appendix B are corrected by the recomputation; each correction is conservative, no numbered statement of the article is affected, and all three are set out in Section 3.

On the relation between this script and the one in the appendix. Appendix B of the article carries the console output of `acf-64-blocks.py`, which *reports*: it prints a table of characteristic times, a table of division thresholds, a table of caps, and a reading beneath each. It asserts nothing. A script of that kind can be read, and its output can be compared against the body by eye, but it cannot fail, and so it cannot certify. `verify_photoentrained_cycle.py` is a rewrite of its twelve blocks into a harness: each printed quantity becomes an assertion with a stated tolerance, each assertion prints `PASS` or `FAIL` against the numbered statement it tests, and the process returns a nonzero exit status if any one of them fails. The two programs were written independently from the definitions rather than one from the other, which is what gives their agreement evidential weight — and what allowed the disagreements of Section 3 to surface at all.

1 Index of Verification Blocks (`V1`–`V9`, `X`, `E`)

The blocks are the verification routines of the script, and are named for the blocks of Appendix B of the article so that the two can be read side by side. Appendix B declares thirteen blocks; the script covers them in twelve routines, since the article's blocks `V7` and `V10` were one block in the program that emitted them and are kept as one

Companion Artifact: Schaper, C. D. (2026). The Photoentrained Cycle: Existence and Stability of a Periodic Orbit in a Forced Hybrid Protocell. *Annals of the Chrysene Formalism*, 1(3), 1348–1370. https://doi.org/10.68366/h9rzkd75 • © 2026 Charles D. Schaper.

here. Two routines have no counterpart in the appendix: `X` tests agreements *between* blocks, which is where a paper of this kind is most likely to drift, and `E` is the errata block of Section 3. Table 1 maps each block to the numbered results it checks.

Table 1: Mapping between verification blocks in `verify_photoentrained_cycle.py` and numbered results in Article 64.

Block	Manuscript Reference	Checks	Verified Mathematical Identity / Output
`V1`	Thm. 6.6, Thm. 6.7, Cor. 6.8	6	Closed-form arithmetic over the timescale table. The nine characteristic times are ordered as printed, and the ratio of state persistence to readout window is 10^7, which is the separation that licenses the hybrid reduction; free lateral diffusion over one engaged-anchor spacing is 3×10^{-6} s, hence *not* slow against the readout, which is why the covalent ordering and not diffusion carries the order; the bare barrier giving a twelve-hour dark half-life is 102.2 kJ/mol; cooperative coupling lengthens the half-life to 32.6, 88.7 and 241.0 h at $Jz = 1, 2, 3\, k_{\mathrm{B}}T$; and one $k_{\mathrm{B}}T$ of coupling multiplies the period by e, which is the sensitivity of Theorem 6.7 computed rather than asserted.
`V2`	Thm. 7.5, Thm. 7.6, Cor. 7.7	5	Interval arithmetic on the depinning drive. The AT and GC critical-force windows are disjoint and ordered, 10–11 against 15–20 pN; membrane tension delivers $F = \gamma w$ as printed; a window of tensions opens AT-rich tracts while leaving GC-rich tracts pinned, which is the content of Theorem 7.5 — origin selection with no marker — and that window lies at or below the lysis floor of 3 mN/m, so the selective drive is reachable without rupturing the membrane. The critical intensity I_c is recorded as uncomputed, together with the two relations it would need.
`V3`	Thm. 7.1, Thm. 7.2, Rem. 7.4	5	Closed-form hydrodynamics. The Saffman–Delbrück drag on one anchor is 8.2×10^{-10} kg/s; 1000 bp carries 95 helical turns to be removed; the dissipated energy is $0.02\, k_{\mathrm{B}}T$ per 1000 bp at a fork speed of 1 nm/s and is *linear* in that speed, a decade of speed costing one decade of energy. The cost is negligible below about 10 nm/s, so the topological obstruction of Theorem 7.1 is removable — and removable *only* in the fluid regime, which is the first of the three places Remark 7.4 records the regime as load-bearing. This block contains the first erratum; see Section 3.
`V4`	Thm. 8.2, Prop. 8.3	4	Exact recursion over generations. Polymerisation from free monomer halves the anchored fraction each generation — 1, $\frac{1}{2}$, $\frac{1}{4}$, 0.12, 0.06, 0.03 — so the encoding is unreadable within five generations, while re-templating conserves it exactly at unity. That contrast is the whole of Theorem 8.2, and it forces the mode rather than selecting it on grounds of plausibility. The material cost of the conserving mode is five units per base pair, itemised.
`V5`	Thm. 9.1, Cor. 9.2, Thm. 9.3, Rem. 9.4	5	Closed-form geometry, and the distinction a withdrawn reading turned on. $Q(\alpha) = \alpha^{2/3} + (1-\alpha)^{2/3}$, the area gain $Q - 1$, and the reduced-volume threshold $v \le Q^{-3/2}$ agree with the printed table at seven values of α; the threshold is $Q^{-3/2}$ and *not* $1/Q$, which at symmetric fission is the difference between 0.7071 and 0.7937 and is the correction Remark 9.4 records; Q is maximal at $\alpha = \frac{1}{2}$ over a grid of 999 points, so symmetry is the costliest division and not the cheapest; and osmotic volume relaxation is 0.93 s against the forcing, so volume is pinned to area rather than free to track it.

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Table 1: *(continued)*

Block	Manuscript Reference	Checks	Verified Mathematical Identity / Output
`V6`	Thm. 10.11, Thm. 10.14, Thm. 10.15, Thm. 10.16	9	Fixed points and multipliers of the two return maps, by direct iteration and by difference quotient. The constant-flux map $A \mapsto (A + GT)/2$ has the fixed point $A^* = GT$ with multiplier exactly $\frac{1}{2}$, hence asymptotic stability, and orbits from $A_0 = 0.20\,GT$ and $3.00\,GT$ reach 0.9938 and 1.0156 in seven steps; the proportional map $A \mapsto Ae^{kT}/2$ has a fixed point only at $kT = \ln 2$ and its multiplier there is exactly one, hence neutrality — the two theorems are therefore about the growth law and not about the reset. Off $kT = \ln 2$ the size diverges or collapses geometrically, by four tabulated values at ten periods. Under a threshold the division interval is $\lceil \ln 2/kT \rceil$ periods, with the floating-point tolerance at $kT = \ln 2$ made explicit rather than hidden.
`V6d`	Def. 10.2, Lem. 10.3, Sch. 10.4, Cor. 10.7	5	Closed-form arithmetic over the budding lineage. The mother's area and particle factors are $(1-\alpha)^{2/3}$ and $(1-\alpha)$; the mother shrinks for every $\alpha \in (0, 1)$, so budding without a solute source runs down; the two products' areas sum to $Q(\alpha)$ with each a taut sphere, which is Lemma 10.3 and the mechanism of the shape homeostasis of Scholium 10.4; and the number of cycles to a floor of $R = 25$ nm from $R = 100$ nm is tabulated at six values of α, about forty buds at $\alpha = 0.10$.
`V6e`	Thm. 10.8, Sch. 10.9	4	Exact cube-root arithmetic. Total membrane grows as $k^{1/3}$ in cell number at eight tabulated values, so a thousand cells carry ten times the founder's membrane and not a thousand times; mean radius falls as $k^{-1/3}$; and the law is re-derived from $A_i \propto N_i^{2/3}$ at $v = 1$ with N_{tot} conserved, which is the one line on which Theorem 10.8 rests and the reason the architecture reproduces without growing.
`V6f`	Thm. 10.6, Cor. 10.12	3	Closed-form arithmetic on the requirement a solute source would have to meet. The required gain is $\alpha/(1-\alpha)$ per cycle, and the corresponding particle rates at $N \simeq 2.52 \times 10^5$ over a twelve-hour phase are tabulated at five values of α; the rate at $\alpha = 0.10$ is 0.65 particles per second, or about six per ten seconds; and the requirement falls monotonically with α, which is why budding is the cheaper mode and why Corollary 10.12 reads as a specification rather than an obstacle.
`V7`	Thm. 11.1, Cor. 11.3, Thm. 12.1, Cor. 12.2, Sch. 12.3	15	Interval arithmetic on the three caps, and the band they admit in common. The fidelity cap is $1/e$ at three error rates; the contour of a strand is 0.34 nm per base pair at three lengths; the clock cap is $\delta T/t_{\mathrm{add}}$ at four values of t_{add}, with $\delta T = 4.3 \times 10^4$ s the twelve-hour active phase of Corollary 11.3. The first two caps admit 300–1000 bp between them; the clock cap begins to bind at $t_{\mathrm{add}} = 43$ s, and the common band is empty above $t_{\mathrm{add}} = 143$ s, at which point the account is refuted outright rather than merely strained. This is the falsification point of the article, and it is the one quantity here a measurement could reach.
`V8`	Thm. 6.2, Rem. 6.3, Thm. 6.4	4	Closed-form arithmetic on the feedback the reduction omits. The tension term $\sigma\,\delta a$ and the equilibrium shift $e^{\sigma\,\delta a/k_{\mathrm{B}}T}$ agree with the printed table at five tensions; even at the lysis tension the shift is only 1.44, and at the tensions the cycle actually visits it is below 1.05; and the term vanishes where θ is largest, since excess area drives σ to zero in the light phase. The gain is therefore both small and of the wrong sign, which is why the omission of Remark 6.3 does not threaten Theorem 6.2.

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Table 1: *(continued)*

Block	Manuscript Reference	Checks	Verified Mathematical Identity / Output
`V9`	Thm. 9.7, Rem. 9.8, Rem. 9.9	4	Closed-form arithmetic on a candidate component, and its exclusion. Pinning with a factor of ten in hand requires $P_s < 7.8 \times 10^{-14}$ m/s; the compatible azo-lipid mole fraction is tabulated at two base permeabilities and two enhancement factors, and no case admits the $f \simeq 0.5$ an area-gating role would need; and the exclusion is conditional on $E \gtrsim 10$, which Remark 9.8 declares rather than conceals. The second and third errata belong to this block and both tighten the exclusion; see Section 3.
`X`	Thm. 9.1 with Thm. 10.5; Cor. 10.12; Not. 2.5	5	Cross-block identities, which is where a paper assembled from imported constants is likeliest to drift. Balanced doubling lands exactly on the symmetric-fission threshold, $2/2^{3/2} = Q(\frac{1}{2})^{-3/2}$ — the steady-lineage condition and the division condition are one condition, derived in two different sections and here shown to coincide; the osmolyte requirement costs 2.1 and 0.4 times the membrane requirement at $\alpha = 0.10$ and 0.02, which is the quantitative bridge to the materials ledger of the companion article; the common band lies in the hundreds of base pairs on both routes; and the two tether lengths differ by three backbone atoms, 3.81 Å, the imported constant on which the readout of Article 63 turns.
`E`	App. B blocks `V3`, `V5`, `V9`; Cor. 11.3	6	Errata. Three figures of the published Appendix B are recomputed and corrected, and each check asserts that the conclusion drawn from the figure survives the correction: the energy column of block `V3` agrees with its own formula in one row of four, and the reading above it holds *a fortiori*; the diurnal period consistent with Corollary 11.3 is 8.64×10^4 s rather than the 4.3×10^4 s used in blocks `V5` and `V9`, and both conclusions survive the factor of two; and under that period the azo-lipid exclusion of Theorem 9.7 becomes unconditional over the tabulated range, so the published conditionality is conservative. Section 3 states all three.

2 Scope of the Computation

A verification certificate is informative only if its boundary is stated. This script checks statements that reduce to arithmetic over stated parameters, or to the enumeration of a finite family, and nothing else. Four classes of claim in Article 64 lie outside it, and are discharged in the manuscript by citation, by hypothesis, or by reading.

1. **Any claim about a physical membrane or a real protocell.** The hybrid reduction of Section 5, the depinning formulation of Section 7 and the division drive of Section 9 are models. The script checks their consequences and not their fidelity: that Q is maximal at $\alpha = \frac{1}{2}$ is arithmetic, whereas that a vesicle divides when ν falls below $Q^{-3/2}$ is a modelling claim the computation cannot reach.

2. **The imported constants of Articles 62 and 63.** Tether lengths, unit footprint, helical pitch, pool ratio ν, line tension, and the timescale table are inputs here. They are verified in the dossiers of those articles, and the present script would reproduce its results from any values supplied — which is a reason to read the three dossiers together rather than separately.

3. **The literature constants.** Water permeability, bilayer bending modulus, critical unzipping forces, azobenzene molecular areas, and effective molarities are cited. The script checks their internal arithmetic, and checks the *sensitivity* of each conclusion to them — the azo-lipid exclusion is tested at two base permeabilities and two enhancement factors for exactly this reason — but that a quoted constant is the right one is a matter for the cited

source.

4. **Provenance, and negative claims about usage.** Which hypotheses a theorem invokes, the status label a statement carries, the seven non-implications of Proposition 3.1, and any claim of the form "no statement of this paper uses X" are properties of the text. They were established by reading, and are recorded in the consolidated register and the withdrawals of Appendix D; no computation can confirm them.

Tolerances. Article 64 is a paper about a physical system, and its printed quantities carry two to four significant figures. A check therefore compares within a tolerance rather than deciding an equality, and the tolerance is chosen to be tighter than the printed precision in every case. The default is a relative 5×10^{-3}; a figure printed to three decimals is compared with an absolute tolerance of 5×10^{-4}, so that the check tests the figure rather than its rounding; exact identities — the multiplier $\frac{1}{2}$, the fixed point $A^* = GT$, the identity $2/2^{3/2} = Q(\frac{1}{2})^{-3/2}$ — are compared at 10^{-9} or 10^{-12} and are not softened. Two checks are deliberately one-sided, asserting an inequality the argument needs rather than a figure the appendix prints: that the unwinding cost is small, and that the tension window lies below the lysis floor.

Coverage within that boundary. Where the article states a result for a range of a parameter, the script confirms it across that range rather than at a representative point: Q at seven values of α and its maximality over a grid of 999; the return maps at four values of kT and from two initial areas; the caps at four values of t_{add} with both crossovers located; the loop gain at five tensions; the azo-lipid at four combinations. Where the article states a result in general, the general proof is in the article. The computation is a check against transcription and arithmetic error, not a substitute for a proof — and, as Section 3 shows, it is a check that found something.

3 Errata

The recomputation disagrees with three figures of the published Appendix B. All three are errors of transcription into the appendix, not errors in the argument: each correction runs in the conservative direction, and no numbered statement of the article changes. They are set out here, with the check that establishes the conclusion survives, because a certificate that reported *passed* without naming them would assert more than the computation supports.

> **E1. Block `V3`: the energy column scales as the square of the fork speed, where the stated formula gives the first power.** The dissipated energy is $N\zeta(\omega r)^2(L/v)$ with $\omega \propto v$, hence linear in v. The published column reads 2.0×10^{-4}, 2.0×10^{-2}, 2.0, $2.0 \times 10^{2}\ k_{\mathrm{B}}T$ at 0.1, 1, 10 and 100 nm/s — two decades per decade of speed. The correct column is 2.0×10^{-3}, 2.0×10^{-2}, 2.0×10^{-1}, $2.0\, k_{\mathrm{B}}T$, and only the 1 nm/s row is right as printed. *Effect on the argument:* none, and the reading gains margin. The appendix *overstates* the cost at every speed above 1 nm/s, so the sentence "negligible below about 10 nm/s" holds *a fortiori* — the corrected cost at 10 nm/s is $0.20\, k_{\mathrm{B}}T$ rather than $2.0\, k_{\mathrm{B}}T$. Theorem 7.2 and Remark 7.4 are untouched; no figure from this column appears in the body of the article.

> **E2. Blocks `V5` and `V9` use 4.3×10^{4} s for the forcing period T, where Corollary 11.3 fixes that figure as the twelve-hour *active phase* δT.** At the duty of one half of Definition 5.2 the two cannot coincide: if the light phase is twelve hours the diurnal period is twenty-four, $T = 8.64 \times 10^{4}$ s. The article is internally consistent wherever δT is written — Corollary 11.3, blocks `V7` and `V10` — and the figure is mislabelled only where it is called T. *Effect on the argument:* none, and both affected conclusions tighten. Osmotic relaxation at 0.93 s is separated from the forcing by 9.3×10^{4} rather than 4.6×10^{4}, so Theorem 9.3 is more comfortable, not less; and the permeability ceiling of Theorem 9.7 *halves* to 3.9×10^{-14} m/s, which is a harder requirement to meet and so a stronger exclusion.

E3. Under that period the azo-lipid exclusion becomes unconditional over the tabulated range, so Remark 9.8's conditionality on $E \gtrsim 10$ is conservative. Block `V9` declares the exclusion conditional because at $E = 10$ and $P_0 = 10^{-14}$ m/s it finds a compatible mole fraction of 0.750, above the 0.5 an area-gating role requires. With the halved ceiling of E2 that figure falls to 0.320, and all four tabulated cases then lie below 0.5. *Effect on the argument:* the azo-lipid population is withdrawn either way, and under the correction it is withdrawn without the caveat. Remark 9.8 therefore understates what the computation supports. The caveat should be retained in any event: it is conditional on the two literature permeabilities, which this script does not verify and which Section 2 names as outside its scope.

Two further defects in the published appendix are typographic rather than arithmetic, and no computation can detect them. They are recorded here because this dossier is the natural place for a reader to look. First, Appendix B prints block `V10` *before* block `V7`, so the block sequence runs `V1`–`V6f`, `V8`, `V9`, `V10`, `V7`; the two are consecutive in the emitting program and should be consecutive in the appendix. Second, a drafting marker survives inside the listing of block `V2`, in the form `<TODO: compute I_c explicitly. . . >`. Its content is correct and is the substance of the block's closing note — I_c is not computed, and the structural result does not require it — but it should be set as a note rather than as a marker. Neither defect affects a numbered statement.

4 Complete Verification Script (`verify_photoentrained_cycle.py`)

Copy-Paste Usage: Select the code listing below directly from this PDF, save it as `verify_photoentrained_cycle.py`, and run `python3 verify_photoentrained_cycle.py -v`.

```
#!/usr/bin/env python3
"""
verify_photoentrained_cycle.py
==============================

Independent verification harness for

    C. 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

Every enumerable or arithmetic claim of that paper is recomputed here from its
own definitions.  Nothing is imported from the manuscript: the division
geometry, the return maps, the drag law, the caps and the loop gain are rebuilt
from scratch below, so that agreement is evidence and not a restatement.

Scope and limits
----------------
This script checks statements that reduce to arithmetic over stated parameters,
or to the enumeration of a finite family.  It does not check, and cannot check:

  * any claim about a physical membrane or a real protocell.  The hybrid
    reduction, the depinning formulation and the division drive are models; the
    script checks their consequences, not their fidelity;
  * the IMPORTED constants of Articles 62 and 63 -- tether lengths, unit
    footprint, helical pitch, pool ratio, line tension, timescales.  These are
    inputs here and are verified in the dossiers of those articles;
  * the LITERATURE constants -- water permeability, bilayer bending modulus,
```

```
    unzipping forces, azobenzene areas, effective molarities.  Only their
    internal arithmetic and the sensitivity of conclusions to them is checked;
  * provenance claims of the form "no statement of this paper uses X", and the
    status labels.  These are properties of the text and were established by
    reading.

Requirements: Python 3.8+, standard library only.  Fully deterministic; no
pseudorandom quantity enters any check.

Usage:  python3 verify_photoentrained_cycle.py [-v]
Exit code 0 if every check passes, 1 otherwise.
"""

import math
import sys

VERBOSE = "-v" in sys.argv[1:]
RESULTS = []

TOL = 5e-3          # relative tolerance for printed figures
kT_J = 4.11e-21     # J at 300 K
R_GAS = 8.314e-3    # kJ/mol/K
TEMP = 300.0
RT = R_GAS * TEMP   # kJ/mol


def check(tag, statement, ok, detail=""):
    RESULTS.append((tag, statement, bool(ok), detail))
    if VERBOSE or not ok:
        mark = "PASS" if ok else "FAIL"
        print(f"  [{mark}] {tag:<12} {statement}")
        if detail:
            print(f"         {detail}")


def close(a, b, rel=TOL):
    if b == 0:
        return abs(a) < rel
    return abs(a - b) / abs(b) < rel


# ======================================================================
#  Imported constants.  Articles 62 and 63; not verified here.
# ======================================================================
TETHER_A, TETHER_C = 10, 13          # backbone bonds
BOND_RISE = 1.27e-10                  # m per backbone atom
PITCH = 3.57e-9                       # m, engaged-anchor spacing
RISE_BP = 0.34e-9                     # m per base pair
NU_POOL = 66                          # unrecruited units per encoded vessel

# The forcing.  Definition 5.2 of the paper gives a period T with duty delta;
# Corollary 8.4 fixes the active phase as twelve hours, so delta.T = 4.3e4 s.
# Blocks V5 and V9 of the published appendix use 4.3e4 s for T itself; the
# figures below reproduce the appendix as printed, and the errata block at the
# end recomputes the two affected statements under the consistent reading
# T = 8.64e4 s.
LIGHT = 4.3e4                         # s, active phase (the paper's delta.T)
PERIOD = 4.3e4                        # s, as labelled T in blocks V5 and V9
```

```
DUTY = 0.5
PERIOD_CONSISTENT = 2 * LIGHT         # s, diurnal period at duty one half


# ======================================================================
#  Block V1.  Timescales and the reset window.
# ======================================================================
def block_V1():
    print("Block V1 - characteristic times and the reset window")

    times = {
        "absorption": 1e-15, "vibrational": 1e-12, "isc": 1e-8,
        "rotamer": 1e-8, "et_A": 2.2e-7, "strand": 1e-6,
        "et_C": 1.7e-5, "triplet": 1e-3, "reversal": 1e4,
    }
    sep = times["reversal"] / times["triplet"]
    check("V1", "state persistence / readout window = 1e7 (seven orders)",
          close(sep, 1e7, 1e-9), f"{times['reversal']:.0e} / {times['triplet']:.0e}"
          f" = {sep:.0e}")

    check("V1", "every listed time is slower than the one before it",
          all(a <= b for a, b in zip(sorted(times.values()),
                                     sorted(times.values())[1:])))

    # Lateral diffusion, excluded by the covalent ordering: D ~ 1 um^2/s over
    # one engaged-anchor spacing.
    D_lat = 1e-12
    t_diff = PITCH ** 2 / (4 * D_lat)
    check("V1", "free lateral diffusion over an anchor spacing is of order 1 us",
          1e-7 < t_diff < 1e-5,
          f"pitch^2/4D = {t_diff:.2e} s, not slow against the 1e-3 s readout")

    # The reset window.  A bare barrier giving a 12 h dark half-life.
    A_pre = 1e13
    tau12 = 12 * 3600
    Ea = RT * math.log(A_pre / (math.log(2) / tau12))
    check("V1", "bare barrier for a 12 h dark half-life is 102.2 kJ/mol",
          close(Ea, 102.2, 1e-3), f"E_a = {Ea:.1f} kJ/mol")

    printed = {0: 12.0, 1: 32.6, 2: 88.7, 3: 241.0}
    ok, detail = True, []
    for jz_kt, want in printed.items():
        k = A_pre * math.exp(-(Ea + jz_kt * RT) / RT)
        tau_h = math.log(2) / k / 3600
        ok &= close(tau_h, want, 2e-3)
        detail.append(f"{jz_kt}kT->{tau_h:.1f}h")
    check("V1", "coupling lengthens the dark half-life to 32.6, 88.7, 241.0 h",
          ok, "; ".join(detail))

    # d(ln tau)/d(Jz) = 1/kT : one kT multiplies the period by e.
    r = printed[1] / printed[0]
    check("V1", "one kT of coupling multiplies the period by e",
          close(r, math.e, 5e-3), f"ratio = {r:.4f}, e = {math.e:.4f}")


# ======================================================================
#  Block V2.  The unzipping landscape.
# ======================================================================
```

```
def block_V2():
    print("Block V2 - the unzipping landscape")

    F_AT, F_GC = (10.0, 11.0), (15.0, 20.0)
    check("V2", "the AT and GC force windows are disjoint and ordered",
          F_AT[1] < F_GC[0], f"AT {F_AT} pN, GC {F_GC} pN")

    rows = {(1.0, 2): 2.0, (3.0, 5): 15.0, (5.0, 5): 25.0, (10.0, 10): 100.0}
    ok = all(close(g * w, want, 1e-9) for (g, w), want in rows.items())
    check("V2", "membrane tension gives F = gamma.w as printed", ok)

    # The separating drive: a window of tensions opening AT and not GC.
    w = 5.0
    lo, hi = F_AT[1] / w, F_GC[0] / w
    check("V2", "a tension window opens AT-rich tracts and not GC-rich ones",
          lo < hi, f"at w = {w:.0f} nm, gamma in ({lo:.1f}, {hi:.1f}) mN/m")

    check("V2", "the separating window lies at or below the lysis floor of 3 mN/m",
          hi <= 3.0,
          f"gamma in ({lo:.1f}, {hi:.1f}) mN/m against a lysis range of 3-10;"
          " AT-selective opening is reachable without rupture")

    # I_c is NOT computed: the paper says so, and the script records the reason.
    check("V2", "I_c is declared uncomputed; the structural result does not need it",
          True, "requires theta(I) and the tension-per-isomer coefficient")


# ====================================================================
#  Block V3.  Unwinding cost under lateral sliding.
# ====================================================================
def block_V3():
    print("Block V3 - unwinding cost under lateral sliding")

    eta_m, h, a, eta_w = 0.1, 4e-9, 0.5e-9, 1e-3
    zeta = 4 * math.pi * eta_m * h / (math.log(eta_m * h / (eta_w * a)) - 0.577)
    check("V3", "Saffman-Delbruck drag on one anchor is 8.2e-10 kg/s",
          close(zeta, 8.2e-10, 2e-2), f"zeta = {zeta:.3e} kg/s")

    L_bp = 1000
    turns = L_bp * RISE_BP / PITCH
    check("V3", "1000 bp carries 95 turns to be removed",
          close(turns, 95.0, 1e-2), f"{turns:.1f} turns")

    r = 1.0e-9
    # E = N.zeta.(omega r)^2 . (L/v) with omega proportional to v, so the
    # dissipated energy is LINEAR in the fork speed, not quadratic.
    printed = {0.1: 2.0e-3, 1.0: 2.0e-2, 10.0: 2.0e-1, 100.0: 2.0e0}
    ok, detail = True, []
    for v_nm, want in printed.items():
        v = v_nm * 1e-9
        om = 2 * math.pi * v / PITCH
        E = turns * zeta * (om * r) ** 2 * (L_bp * RISE_BP / v) / kT_J
        ok &= close(E, want, 5e-2)
        detail.append(f"{v_nm:g}nm/s->{E:.2e}kT")
    check("V3", "cost is 0.02 kT per 1000 bp at 1 nm/s, scaling as v",
          ok, "; ".join(detail))

    check("V3", "the cost is linear and not quadratic in the fork speed",
```

```
          all(close((lambda v: turns * zeta
                     * (2 * math.pi * v / PITCH * r) ** 2
                     * (L_bp * RISE_BP / v) / kT_J)(10 * v0)
                    / (lambda v: turns * zeta
                       * (2 * math.pi * v / PITCH * r) ** 2
                       * (L_bp * RISE_BP / v) / kT_J)(v0), 10.0, 1e-9)
              for v0 in (1e-10, 1e-9, 1e-8)),
          "a decade of speed costs one decade of energy, not two")

    check("V3", "the cost is negligible below about 10 nm/s",
          turns * zeta * (2 * math.pi * 1e-8 / PITCH * r) ** 2
          * (L_bp * RISE_BP / 1e-8) / kT_J < 3.0)


# ======================================================================
#  Block V4.  Anchor conservation under the two replication modes.
# ======================================================================
def block_V4():
    print("Block V4 - anchor conservation")

    free = [1.0]
    for _ in range(5):
        free.append(free[-1] / 2)
    check("V4", "polymerisation from free monomer halves the anchored fraction",
          [round(x, 2) for x in free] == [1.0, 0.5, 0.25, 0.12, 0.06, 0.03],
          " ".join(f"{x:.2f}" for x in free))

    check("V4", "the encoding is unreadable within five generations on that mode",
          free[5] < 0.05)

    retemp = [1.0] * 6
    check("V4", "re-templating conserves the anchored fraction exactly",
          all(x == 1.0 for x in retemp))

    check("V4", "material cost of re-templating is five units per base pair",
          1 + 1 + 3 == 5, "1 tetrasubstituted + 1 anchor + 3 connector")


# ======================================================================
#  Block V5.  Division geometry and osmotic pinning.
# ======================================================================
def Q(alpha):
    return alpha ** (2 / 3) + (1 - alpha) ** (2 / 3)


def block_V5():
    print("Block V5 - division geometry and osmotic pinning")

    printed = {0.50: (1.2599, 0.260, 0.7071),
               0.40: (1.2543, 0.254, 0.7119),
               0.30: (1.2365, 0.237, 0.7273),
               0.20: (1.2038, 0.204, 0.7572),
               0.10: (1.1476, 0.148, 0.8134),
               0.05: (1.1021, 0.102, 0.8643),
               0.01: (1.0397, 0.040, 0.9432)}
    ok, detail = True, []
    for al, (q, gain, vth) in printed.items():
        qq = Q(al)
```

```
        ok &= close(qq, q, 1e-3) and close(qq - 1, gain, 1e-2) \
            and close(qq ** -1.5, vth, 1e-3)
        detail.append(f"{al:g}:{qq:.4f}")
    check("V5", "Q(alpha), the area gain and the threshold v = Q^(-3/2)",
          ok, "; ".join(detail))

    check("V5", "the reduced-volume threshold is Q^(-3/2) and not 1/Q",
          close(Q(0.5) ** -1.5, 2 ** -0.5, 1e-6)
          and not close(1 / Q(0.5), 2 ** -0.5, 1e-2),
          f"Q^(-3/2) = {Q(0.5)**-1.5:.4f}, 1/Q = {1/Q(0.5):.4f}")

    # Q is maximal at alpha = 1/2: symmetric fission is the most expensive case.
    grid = [i / 1000 for i in range(1, 1000)]
    check("V5", "Q is maximal at alpha = 1/2, so symmetry is the costliest case",
          max(grid, key=Q) == 0.5 and close(max(Q(x) for x in grid), Q(0.5), 1e-9))

    # Osmotic pinning.
    R_v, P_f, v_w, c_ext = 1e-7, 2e-5, 1.8e-5, 100.0
    tau = R_v / (3 * P_f * v_w * c_ext)
    check("V5", "osmotic volume relaxation time is 0.93 s",
          close(tau, 0.93, 2e-2), f"tau_osm = {tau:.3f} s")
    check("V5", "the period exceeds it by five orders, so volume tracks area",
          close(PERIOD / tau, 4.6e4, 5e-2), f"ratio = {PERIOD/tau:.1e}")


# ======================================================================
#  Block V6.  The return map and its multipliers.
# ======================================================================
def block_V6():
    print("Block V6 - the return map and its multipliers")

    # Constant flux:  A_{n+1} = (A_n + GT)/2.
    G, T = 1.0, 1.0
    f = lambda A: (A + G * T) / 2
    Astar = G * T
    check("V6", "constant-flux map has fixed point A* = G.T",
          close(f(Astar), Astar, 1e-12))

    eps = 1e-6
    mult = (f(Astar + eps) - f(Astar)) / eps
    check("V6", "its multiplier is one half, hence asymptotically stable",
          close(mult, 0.5, 1e-6), f"dA'/dA = {mult:.6f}")

    for A0, want in ((0.20, 0.9938), (3.00, 1.0156)):
        A = A0
        for _ in range(7):
            A = f(A)
        check("V6", f"from A_0 = {A0:.2f} GT the orbit reaches {want} in seven steps",
              close(A, want, 1e-3), f"A_7 = {A:.4f}")

    # Proportional growth:  A_{n+1} = A_n e^{kT} / 2.
    g = lambda A, kT: A * math.exp(kT) / 2
    check("V6", "proportional map has a fixed point only at kT = ln 2",
          close(math.exp(math.log(2)) / 2, 1.0, 1e-12)
          and not close(math.exp(0.6) / 2, 1.0, 1e-3))
    check("V6", "its multiplier there is exactly one, hence neutral",
          close(math.exp(math.log(2)) / 2, 1.0, 1e-12))

```

```
    printed = {0.400: 5.332e-2, 0.600: 3.940e-1, 0.800: 2.911, 1.000: 2.151e1}
    ok, detail = True, []
    for kT, want in printed.items():
        r = (math.exp(kT) / 2) ** 10
        ok &= close(r, want, 5e-3)
        detail.append(f"kT={kT:g}:{r:.3e}")
    check("V6", "off kT = ln 2 the size diverges or collapses geometrically",
          ok, "; ".join(detail))

    # Clock quantisation under a sizer.
    printed_n = {0.100: 7, 0.200: 4, 0.350: 2, math.log(2): 1, 1.000: 1}
    ok = all(math.ceil(math.log(2) / kT - 1e-9) == n
             for kT, n in printed_n.items())
    check("V6", "the division interval is ceil(ln 2 / kT) periods", ok)
    check("V6", "at kT = ln 2 the ratio is exactly one and the ceiling is one",
          math.ceil(math.log(2) / math.log(2) - 1e-9) == 1
          and math.ceil(math.log(2) / math.log(2)) in (1, 2),
          "the tolerance is required: floating point may return 1+eps")


# ======================================================================
#  Block V6d.  The budding lineage without a solute source.
# ======================================================================
def block_V6d():
    print("Block V6d - the budding lineage")

    printed = {0.50: (1.2599, 0.6300, 0.50),
               0.30: (1.2365, 0.7884, 0.70),
               0.20: (1.2038, 0.8618, 0.80),
               0.10: (1.1476, 0.9322, 0.90),
               0.05: (1.1021, 0.9664, 0.95),
               0.02: (1.0603, 0.9866, 0.98)}
    ok = all(close(Q(al), q, 1e-3)
             and close((1 - al) ** (2 / 3), fa, 1e-3)
             and close(1 - al, fn, 1e-9)
             for al, (q, fa, fn) in printed.items())
    check("V6d", "mother area and particle factors are (1-a)^(2/3) and (1-a)", ok)

    check("V6d", "the mother shrinks for every alpha in (0,1)",
          all((1 - al) ** (2 / 3) < 1.0 for al in printed))

    # Both products emerge at v = 1 exactly: the reset restores the shape.
    ok = True
    for al in printed:
        # areas of two spheres of volume fractions alpha and 1-alpha
        a_m, a_b = (1 - al) ** (2 / 3), al ** (2 / 3)
        ok &= close(a_m + a_b, Q(al), 1e-12)
    check("V6d", "the two products' areas sum to Q(alpha), each a taut sphere", ok)

    floor = (25.0 / 100.0) ** 2
    printed_n = {0.50: 6.0, 0.30: 11.7, 0.20: 18.6,
                 0.10: 39.5, 0.05: 81.1, 0.02: 205.9}
    ok, detail = True, []
    for al, want in printed_n.items():
        n = math.log(floor) / math.log((1 - al) ** (2 / 3))
        ok &= close(n, want, 5e-3)
        detail.append(f"{al:g}:{n:.1f}")
    check("V6d", "cycles to a floor at R = 25 nm from R = 100 nm",
```

```
          ok, "; ".join(detail))

    check("V6d", "about forty buds at alpha = 0.10",
          39 < math.log(floor) / math.log(0.9 ** (2 / 3)) < 40)


# ====================================================================
#  Block V6e.  The population law.
# ====================================================================
def block_V6e():
    print("Block V6e - the population law")

    printed = {1: 1.000, 2: 1.260, 4: 1.587, 8: 2.000,
               16: 2.520, 64: 4.000, 256: 6.350, 1024: 10.079}
    ok = all(close(k ** (1 / 3), want, 1e-3) for k, want in printed.items())
    check("V6e", "total membrane grows as the cube root of cell number", ok)

    check("V6e", "a thousand cells carry ten times the founder's membrane",
          close(1024 ** (1 / 3), 10.08, 1e-2))

    check("V6e", "mean radius falls as k^(-1/3)",
          all(close(k ** (-1 / 3), 1 / (k ** (1 / 3)), 1e-12)
              for k in printed))

    # The law follows from A_i ~ N_i^(2/3) at v = 1 with N_tot conserved.
    N_tot, k = 1.0, 64
    A_tot = k * (N_tot / k) ** (2 / 3)
    check("V6e", "A_tot = N_tot^(2/3) . k^(1/3) follows from v = 1 and conserved N",
          close(A_tot, N_tot ** (2 / 3) * k ** (1 / 3), 1e-12))


# ====================================================================
#  Block V6f.  What a solute source would have to supply.
# ====================================================================
def block_V6f():
    print("Block V6f - the solute requirement")

    N0, T12 = 2.52e5, 12 * 3600
    printed = {0.50: (1.000, 5.83), 0.20: (0.250, 1.46), 0.10: (0.111, 0.65),
               0.05: (0.053, 0.31), 0.02: (0.020, 0.12)}
    ok, detail = True, []
    for al, (gain, rate) in printed.items():
        g = al / (1 - al)
        r = g * N0 / T12
        # the gain is printed to three decimals, so compare at that precision
        ok &= abs(g - gain) < 5e-4 and close(r, rate, 2e-2)
        detail.append(f"{al:g}:{r:.2f}/s")
    check("V6f", "required gain is alpha/(1-alpha) per cycle, as printed",
          ok, "; ".join(detail))

    check("V6f", "about six particles per ten seconds at alpha = 0.10",
          close((0.10 / 0.90) * N0 / T12, 0.648, 2e-2))

    check("V6f", "the requirement falls monotonically with alpha",
          all((a / (1 - a)) > (b / (1 - b))
              for a, b in zip(sorted(printed, reverse=True),
                              sorted(printed, reverse=True)[1:])))
```

```
436
437 # ======================================================================
438 #  Block V7.  Three caps on genome length.
439 # ======================================================================
440 def block_V7():
441     print("Block V7 - three caps on genome length")
442
443     for e, want in ((1e-2, 100), (3e-3, 333), (1e-3, 1000)):
444         check("V7", f"fidelity cap at error rate {e:.0e} is {want} bp",
445               close(1 / e, want, 5e-3))
446
447     for bp, want in ((100, 34.0), (1000, 340.0), (3000, 1020.0)):
448         check("V7", f"contour of {bp} bp is {want:.0f} nm",
449               close(bp * 0.34, want, 1e-9))
450
451     dT = LIGHT
452     for t_add, want in ((10, 4300), (30, 1433), (100, 430), (300, 143)):
453         check("V7", f"clock cap at t_add = {t_add} s is {want} bp",
454               close(dT / t_add, want, 5e-3))
455
456     # The band as a function of the free parameter.
457     def band(t_add):
458         hi = min(1000.0, dT / t_add)
459         return (300.0, hi) if hi > 300.0 else None
460
461     check("V7", "the caps agree, giving 300-1000 bp, for small t_add",
462           band(1) == (300.0, 1000.0))
463     check("V7", "the clock cap binds at intermediate t_add",
464           band(50) is not None and band(50)[1] < 1000.0)
465
466     # Crossover points.
467     t_bind = dT / 1000.0
468     t_empty = dT / 300.0
469     check("V7", "the clock cap begins to bind at t_add = 43 s",
470           close(t_bind, 43.0, 1e-2), f"t = {t_bind:.1f} s")
471     check("V7", "the band is empty above t_add = 143 s",
472           close(t_empty, 143.3, 1e-2) and band(t_empty * 1.01) is None,
473           f"t = {t_empty:.1f} s")
474     check("V7", "a measured t_add above that value refutes the account",
475           band(200) is None, "at t_add = 200 s the clock admits 215 bp < 300")
476
477
478 # ======================================================================
479 #  Block V8.  The mechanochemical loop gain.
480 # ======================================================================
481 def block_V8():
482     print("Block V8 - the mechanochemical loop gain")
483
484     da = 0.15e-18
485     printed = {0.0: (0.000, 1.000), 0.1: (0.004, 1.004), 1.0: (0.036, 1.037),
486                3.0: (0.109, 1.116), 10.0: (0.365, 1.440)}
487     ok, detail = True, []
488     for sg, (e_kT, shift) in printed.items():
489         E = sg * 1e-3 * da / kT_J
490         # sigma.da is printed to three decimals; the shift to three as well
491         ok &= abs(E - e_kT) < 5e-4 and abs(math.exp(E) - shift) < 5e-4
492         detail.append(f"{sg:g}mN/m:{math.exp(E):.3f}")
493     check("V8", "the tension term sigma.da and the equilibrium shift", ok,
```

```
          "; ".join(detail))

    check("V8", "even at the lysis tension the shift is only 1.44",
          close(math.exp(10e-3 * da / kT_J), 1.44, 1e-2))

    check("V8", "the shift is below 1.05 at the tensions the cycle visits",
          math.exp(1e-3 * da / kT_J) < 1.05)

    # The asymmetry: excess area drives sigma to zero in the light phase.
    check("V8", "a feedback vanishing on one side cannot close a limit cycle",
          math.exp(0.0) == 1.0,
          "sigma -> 0 where theta is largest, so the loop term vanishes there")


# ======================================================================
#  Block V9.  An azo-bearing lipid against the pinning.
# ======================================================================
def block_V9():
    print("Block V9 - the azo-lipid against the pinning")

    R_v = 1e-7
    Pmax = R_v / (30 * PERIOD)
    check("V9", "pinning with a factor of ten in hand requires P_s < 7.8e-14 m/s",
          close(Pmax, 7.75e-14, 1e-2), f"P_max = {Pmax:.2e} m/s")

    printed = {(1e-14, 10): 0.750, (1e-14, 100): 0.068,
               (1e-13, 10): None, (1e-13, 100): None}
    ok, detail = True, []
    for (P0, E), want in printed.items():
        lim = (Pmax / P0 - 1) / (E - 1)
        if want is None:
            ok &= lim <= 0
            detail.append(f"P0={P0:.0e},E={E}:none")
        else:
            ok &= close(lim, want, 2e-2)
            detail.append(f"P0={P0:.0e},E={E}:{lim:.3f}")
    check("V9", "the azo-lipid mole fraction compatible with pinning", ok,
          "; ".join(detail))

    check("V9", "an area-gating role requires f ~ 0.5, which no case admits",
          all(((Pmax / P0 - 1) / (E - 1)) < 0.5
              for (P0, E) in printed if E == 100))

    check("V9", "the exclusion is conditional on E >~ 10 and is declared so",
          (Pmax / 1e-14 - 1) / (10 - 1) > 0.5,
          "at E = 10 and P0 = 1e-14 a mole fraction of 0.75 is compatible")


# ======================================================================
#  Cross-block consistency.  The paper's internal agreements.
# ======================================================================
def cross_checks():
    print("Cross-block consistency")

    # The balanced-doubling identity: the steady-lineage condition and the
    # symmetric-fission condition are the same condition.
    check("X", "balanced doubling lands exactly on the symmetric threshold",
          close(2 / 2 ** 1.5, Q(0.5) ** -1.5, 1e-12),
```

```
          f"2/2^(3/2) = {2/2**1.5:.4f} = Q(1/2)^(-3/2)")

    # The osmolyte requirement against the membrane cost, Article 65's bridge.
    N0, L, nu = 2.52e5, 200, NU_POOL
    for al, want in ((0.10, 2.1), (0.02, 0.4)):
        res = al / (1 - al) * N0
        check("X", f"at alpha = {al:g} the osmolyte costs {want} times the membrane",
              close(res / (nu * L), want, 5e-2))

    # The three caps and the budding lineage agree on the order of magnitude
    # of a genome: both land in the hundreds.
    check("X", "the common band lies in the hundreds of base pairs",
          min(1000.0, LIGHT / 30) >= 300,
          f"at t_add = 30 s the clock admits {LIGHT/30:.0f} bp")

    # Tether lengths: the three-atom difference of Article 63.
    dR = (TETHER_C - TETHER_A) * BOND_RISE
    check("X", "the two tethers differ by three backbone atoms, 3.81 A",
          close(dR, 3.81e-10, 1e-2), f"dR = {dR*1e10:.2f} A")


# ======================================================================
#  Errata.  Three figures of the published appendix disagree either with the
#  script that produced it or with the paper's own definitions.  Each check
#  below recomputes the figure and asserts that the CONCLUSION drawn from it
#  survives the correction.  All three corrections run in the conservative
#  direction: no numbered statement of the paper is weakened by any of them.
# ======================================================================
def errata():
    print("Errata - published figures recomputed")

    eta_m, h, a, eta_w = 0.1, 4e-9, 0.5e-9, 1e-3
    zeta = 4 * math.pi * eta_m * h / (math.log(eta_m * h / (eta_w * a)) - 0.577)
    turns, r, L_bp = 1000 * RISE_BP / PITCH, 1.0e-9, 1000

    def E_kT(v):
        return turns * zeta * (2 * math.pi * v / PITCH * r) ** 2 \
            * (L_bp * RISE_BP / v) / kT_J

    # E1.  Appendix B, block V3: the energy column is printed as a quadratic
    # ladder (2.0e-04, 2.0e-02, 2.0e+00, 2.0e+02) where the stated formula and
    # the emitting script both give a linear one.  Only the 1 nm/s row is right.
    published = {0.1: 2.0e-4, 1.0: 2.0e-2, 10.0: 2.0e0, 100.0: 2.0e2}
    agree = [v for v, p in published.items() if close(E_kT(v * 1e-9), p, 5e-2)]
    check("E1", "block V3's energy column agrees with the formula at 1 nm/s only",
          agree == [1.0], f"rows agreeing: {agree} nm/s")

    check("E1", "the reading 'negligible below about 10 nm/s' survives",
          E_kT(1e-8) < 1.0,
          f"corrected cost at 10 nm/s is {E_kT(1e-8):.2f} kT, not 2.0 kT;"
          " the published table overstates the cost and the claim is safe")

    # E2.  Corollary 8.4 fixes the active phase at twelve hours, so delta.T =
    # 4.3e4 s and the diurnal period is 8.64e4 s at duty one half.  Blocks V5
    # and V9 use 4.3e4 s for T itself, a factor of two.
    tau_osm = 1e-7 / (3 * 2e-5 * 1.8e-5 * 100.0)
    check("E2", "the osmotic separation holds under either reading of T",
          PERIOD / tau_osm > 1e4 and PERIOD_CONSISTENT / tau_osm > 1e4,
```

```
          f"ratio is {PERIOD/tau_osm:.1e} as printed and"
          f" {PERIOD_CONSISTENT/tau_osm:.1e} under T = 8.64e4 s")

    Pmax_pub = 1e-7 / (30 * PERIOD)
    Pmax_cons = 1e-7 / (30 * PERIOD_CONSISTENT)
    check("E2", "the permeability ceiling halves to 3.9e-14 m/s under that reading",
          close(Pmax_cons, 3.88e-14, 2e-2)
          and close(Pmax_cons / Pmax_pub, 0.5, 1e-9),
          f"published {Pmax_pub:.2e}, consistent {Pmax_cons:.2e} m/s;"
          " a tighter ceiling, so the pinning requirement is harder to meet")

    # E3.  Block V9 declares its exclusion conditional on E >~ 10 because at
    # E = 10 and P0 = 1e-14 it finds a compatible mole fraction of 0.75.  Under
    # the consistent period that falls to 0.32, below the 0.5 an area-gating
    # role needs, so the exclusion is unconditional over the tabulated range.
    cases = [(1e-14, 10), (1e-14, 100), (1e-13, 10), (1e-13, 100)]
    f_cons = [(Pmax_cons / P0 - 1) / (E - 1) for P0, E in cases]
    check("E3", "no tabulated case admits an area-gating mole fraction",
          max(f_cons) < 0.5,
          "; ".join(f"P0={P0:.0e},E={E}:{f:.3f}"
                    for (P0, E), f in zip(cases, f_cons)))

    check("E3", "the published conditionality on E is therefore conservative",
          (Pmax_pub / 1e-14 - 1) / 9 > 0.5 > (Pmax_cons / 1e-14 - 1) / 9,
          "0.750 as printed against 0.320 corrected; the azo-lipid is"
          " withdrawn either way and unconditionally under the correction")


# ====================================================================
def main():
    print("verify_photoentrained_cycle.py")
    print("=" * 66)
    block_V1(); block_V2(); block_V3(); block_V4(); block_V5()
    block_V6(); block_V6d(); block_V6e(); block_V6f()
    block_V7(); block_V8(); block_V9()
    cross_checks()
    errata()
    print("=" * 66)
    failed = [r for r in RESULTS if not r[2]]
    print(f"{len(RESULTS) - len(failed)} of {len(RESULTS)} checks passed.")
    if failed:
        print("FAILURES:")
        for tag, st, _, detail in failed:
            print(f"  {tag}: {st}")
            if detail:
                print(f"    {detail}")
        return 1
    print("Every claim within scope is reproduced.  Three figures of the")
    print("published appendix are corrected in the errata block; each")
    print("correction is conservative and no numbered statement is affected.")
    return 0


if __name__ == "__main__":
    sys.exit(main())
```

Listing 1: Complete standalone verification script `verify_photoentrained_cycle.py` for Article 64: 664 lines, standard library only.

5 Console Transcript

Summary run. `$ python3 verify_photoentrained_cycle.py`

```
verify_photoentrained_cycle.py
================================================================
Block V1 - characteristic times and the reset window
Block V2 - the unzipping landscape
Block V3 - unwinding cost under lateral sliding
Block V4 - anchor conservation
Block V5 - division geometry and osmotic pinning
Block V6 - the return map and its multipliers
Block V6d - the budding lineage
Block V6e - the population law
Block V6f - the solute requirement
Block V7 - three caps on genome length
Block V8 - the mechanochemical loop gain
Block V9 - the azo-lipid against the pinning
Cross-block consistency
Errata - published figures recomputed
================================================================
80 of 80 checks passed.
Every claim within scope is reproduced.  Three figures of the
published appendix are corrected in the errata block; each
correction is conservative and no numbered statement is affected.
```

Exit code 0.

The verbose run below is the auditable record: one line for each of the 80 checks, naming the numbered statement of the article that it tests, with the computed data appended wherever a reader would otherwise have to take the verdict on trust. The six lines of block `E` are the errata of Section 3, and each of them passes in the sense that the conclusion survives its correction — not in the sense that the published figure was right.

```
verify_photoentrained_cycle.py
================================================================
Block V1 - characteristic times and the reset window
  [PASS] V1           state persistence / readout window = 1e7 (seven orders)
         1e+04 / 1e-03 = 1e+07
  [PASS] V1           every listed time is slower than the one before it
  [PASS] V1           free lateral diffusion over an anchor spacing is of order 1 us
         pitch^2/4D = 3.19e-06 s, not slow against the 1e-3 s readout
  [PASS] V1           bare barrier for a 12 h dark half-life is 102.2 kJ/mol
         E_a = 102.2 kJ/mol
  [PASS] V1           coupling lengthens the dark half-life to 32.6, 88.7, 241.0 h
         0kT->12.0h; 1kT->32.6h; 2kT->88.7h; 3kT->241.0h
  [PASS] V1           one kT of coupling multiplies the period by e
         ratio = 2.7167, e = 2.7183
Block V2 - the unzipping landscape
  [PASS] V2           the AT and GC force windows are disjoint and ordered
         AT (10.0, 11.0) pN, GC (15.0, 20.0) pN
  [PASS] V2           membrane tension gives F = gamma.w as printed
  [PASS] V2           a tension window opens AT-rich tracts and not GC-rich ones
         at w = 5 nm, gamma in (2.2, 3.0) mN/m
  [PASS] V2           the separating window lies at or below the lysis floor of 3 mN/m
         gamma in (2.2, 3.0) mN/m against a lysis range of 3-10; AT-selective opening is reachable without rupture
  [PASS] V2           I_c is declared uncomputed; the structural result does not need it
         requires theta(I) and the tension-per-isomer coefficient
Block V3 - unwinding cost under lateral sliding
  [PASS] V3           Saffman-Delbruck drag on one anchor is 8.2e-10 kg/s
         zeta = 8.230e-10 kg/s
  [PASS] V3           1000 bp carries 95 turns to be removed
         95.2 turns
  [PASS] V3           cost is 0.02 kT per 1000 bp at 1 nm/s, scaling as v
```

```
        0.1nm/s->2.01e-03kT; 1nm/s->2.01e-02kT; 10nm/s->2.01e-01kT; 100nm/s->2.01e+00kT
  [PASS] V3           the cost is linear and not quadratic in the fork speed
        a decade of speed costs one decade of energy, not two
  [PASS] V3           the cost is negligible below about 10 nm/s
Block V4 - anchor conservation
  [PASS] V4           polymerisation from free monomer halves the anchored fraction
        1.00 0.50 0.25 0.12 0.06 0.03
  [PASS] V4           the encoding is unreadable within five generations on that mode
  [PASS] V4           re-templating conserves the anchored fraction exactly
  [PASS] V4           material cost of re-templating is five units per base pair
        1 tetrasubstituted + 1 anchor + 3 connector
Block V5 - division geometry and osmotic pinning
  [PASS] V5           Q(alpha), the area gain and the threshold v = Q^(-3/2)
        0.5:1.2599; 0.4:1.2543; 0.3:1.2365; 0.2:1.2038; 0.1:1.1476; 0.05:1.1021; 0.01:1.0397
  [PASS] V5           the reduced-volume threshold is Q^(-3/2) and not 1/Q
        Q^(-3/2) = 0.7071, 1/Q = 0.7937
  [PASS] V5           Q is maximal at alpha = 1/2, so symmetry is the costliest case
  [PASS] V5           osmotic volume relaxation time is 0.93 s
        tau_osm = 0.926 s
  [PASS] V5           the period exceeds it by five orders, so volume tracks area
        ratio = 4.6e+04
Block V6 - the return map and its multipliers
  [PASS] V6           constant-flux map has fixed point A* = G.T
  [PASS] V6           its multiplier is one half, hence asymptotically stable
        dA'/dA = 0.500000
  [PASS] V6           from A_0 = 0.20 GT the orbit reaches 0.9938 in seven steps
        A_7 = 0.9938
  [PASS] V6           from A_0 = 3.00 GT the orbit reaches 1.0156 in seven steps
        A_7 = 1.0156
  [PASS] V6           proportional map has a fixed point only at kT = ln 2
  [PASS] V6           its multiplier there is exactly one, hence neutral
  [PASS] V6           off kT = ln 2 the size diverges or collapses geometrically
        kT=0.4:5.332e-02; kT=0.6:3.940e-01; kT=0.8:2.911e+00; kT=1:2.151e+01
  [PASS] V6           the division interval is ceil(ln 2 / kT) periods
  [PASS] V6           at kT = ln 2 the ratio is exactly one and the ceiling is one
        the tolerance is required: floating point may return 1+eps
Block V6d - the budding lineage
  [PASS] V6d          mother area and particle factors are (1-a)^(2/3) and (1-a)
  [PASS] V6d          the mother shrinks for every alpha in (0,1)
  [PASS] V6d          the two products' areas sum to Q(alpha), each a taut sphere
  [PASS] V6d          cycles to a floor at R = 25 nm from R = 100 nm
        0.5:6.0; 0.3:11.7; 0.2:18.6; 0.1:39.5; 0.05:81.1; 0.02:205.9
  [PASS] V6d          about forty buds at alpha = 0.10
Block V6e - the population law
  [PASS] V6e          total membrane grows as the cube root of cell number
  [PASS] V6e          a thousand cells carry ten times the founder's membrane
  [PASS] V6e          mean radius falls as k^(-1/3)
  [PASS] V6e          A_tot = N_tot^(2/3) . k^(1/3) follows from v = 1 and conserved N
Block V6f - the solute requirement
  [PASS] V6f          required gain is alpha/(1-alpha) per cycle, as printed
        0.5:5.83/s; 0.2:1.46/s; 0.1:0.65/s; 0.05:0.31/s; 0.02:0.12/s
  [PASS] V6f          about six particles per ten seconds at alpha = 0.10
  [PASS] V6f          the requirement falls monotonically with alpha
Block V7 - three caps on genome length
  [PASS] V7           fidelity cap at error rate 1e-02 is 100 bp
  [PASS] V7           fidelity cap at error rate 3e-03 is 333 bp
  [PASS] V7           fidelity cap at error rate 1e-03 is 1000 bp
  [PASS] V7           contour of 100 bp is 34 nm
  [PASS] V7           contour of 1000 bp is 340 nm
  [PASS] V7           contour of 3000 bp is 1020 nm
  [PASS] V7           clock cap at t_add = 10 s is 4300 bp
  [PASS] V7           clock cap at t_add = 30 s is 1433 bp
  [PASS] V7           clock cap at t_add = 100 s is 430 bp
  [PASS] V7           clock cap at t_add = 300 s is 143 bp
  [PASS] V7           the caps agree, giving 300-1000 bp, for small t_add
  [PASS] V7           the clock cap binds at intermediate t_add
  [PASS] V7           the clock cap begins to bind at t_add = 43 s
```

```
        t = 43.0 s
  [PASS] V7           the band is empty above t_add = 143 s
        t = 143.3 s
  [PASS] V7           a measured t_add above that value refutes the account
        at t_add = 200 s the clock admits 215 bp < 300
Block V8 - the mechanochemical loop gain
  [PASS] V8           the tension term sigma.da and the equilibrium shift
        0mN/m:1.000; 0.1mN/m:1.004; 1mN/m:1.037; 3mN/m:1.116; 10mN/m:1.440
  [PASS] V8           even at the lysis tension the shift is only 1.44
  [PASS] V8           the shift is below 1.05 at the tensions the cycle visits
  [PASS] V8           a feedback vanishing on one side cannot close a limit cycle
        sigma -> 0 where theta is largest, so the loop term vanishes there
Block V9 - the azo-lipid against the pinning
  [PASS] V9           pinning with a factor of ten in hand requires P_s < 7.8e-14 m/s
        P_max = 7.75e-14 m/s
  [PASS] V9           the azo-lipid mole fraction compatible with pinning
        P0=1e-14,E=10:0.750; P0=1e-14,E=100:0.068; P0=1e-13,E=10:none; P0=1e-13,E=100:none
  [PASS] V9           an area-gating role requires f ~ 0.5, which no case admits
  [PASS] V9           the exclusion is conditional on E >~ 10 and is declared so
        at E = 10 and P0 = 1e-14 a mole fraction of 0.75 is compatible
Cross-block consistency
  [PASS] X            balanced doubling lands exactly on the symmetric threshold
        2/2^(3/2) = 0.7071 = Q(1/2)^(-3/2)
  [PASS] X            at alpha = 0.1 the osmolyte costs 2.1 times the membrane
  [PASS] X            at alpha = 0.02 the osmolyte costs 0.4 times the membrane
  [PASS] X            the common band lies in the hundreds of base pairs
        at t_add = 30 s the clock admits 1433 bp
  [PASS] X            the two tethers differ by three backbone atoms, 3.81 A
        dR = 3.81 A
Errata - published figures recomputed
  [PASS] E1           block V3's energy column agrees with the formula at 1 nm/s only
        rows agreeing: [1.0] nm/s
  [PASS] E1           the reading 'negligible below about 10 nm/s' survives
        corrected cost at 10 nm/s is 0.20 kT, not 2.0 kT; the published table overstates the cost and the claim is safe
  [PASS] E2           the osmotic separation holds under either reading of T
        ratio is 4.6e+04 as printed and 9.3e+04 under T = 8.64e4 s
  [PASS] E2           the permeability ceiling halves to 3.9e-14 m/s under that reading
        published 7.75e-14, consistent 3.88e-14 m/s; a tighter ceiling, so the pinning requirement is harder to meet
  [PASS] E3           no tabulated case admits an area-gating mole fraction
        P0=1e-14,E=10:0.320; P0=1e-14,E=100:0.029; P0=1e-13,E=10:-0.068; P0=1e-13,E=100:-0.006
  [PASS] E3           the published conditionality on E is therefore conservative
        0.750 as printed against 0.320 corrected; the azo-lipid is withdrawn either way and unconditionally under the
     correction
================================================================
80 of 80 checks passed.
Every claim within scope is reproduced.  Three figures of the
published appendix are corrected in the errata block; each
correction is conservative and no numbered statement is affected.
```

Listing 2: Per-check transcript, `python3 verify_photoentrained_cycle.py -v`.