

Positive Recurrence for Single-Linkage Bimolecular Weakly Reversible Stochastic Reaction Networks

Alec Kriebel

Independent researcher

me@aleckriebel.com

ORCID: 0009-0001-9320-500X

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Abstract

Weak reversibility is conjectured to imply positive recurrence for stochastic mass-action systems. For binary networks with one linkage class, this was previously known under the additional requirement that every species occur in a pure unary or pure-double complex. We remove that requirement. For every positive rate vector, the minimal continuous-time Markov chain restricted to each closed communicating class is nonexplosive. Every nonabsorbing class is positive recurrent, while an absorbing singleton carries its point-mass law; hence every closed class admits a unique stationary probability distribution. The proof marks the target of the most recently fired reaction channel and applies a log-factorial potential to the residual population obtained by subtracting that target. Its increment is exactly a target/source falling-factorial ratio, so following the carried target has zero reward. Finite directed paths propagate the negative drift of a rare terminal source. A normalized-log compactification and an exhaustive bimolecular top-complex alternative either supply such a source or produce a stoichiometric invariant that precludes divergence within the class. The result is class-wise and does not address multiple linkage classes or molecularity above two.

Keywords. Stochastic reaction network; systems biology; chemical master equation; positive recurrence; mass-action kinetics; weak reversibility; continuous-time Markov chain; Foster–Lyapunov method.

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1 Introduction

Stochastic reaction networks are continuous-time Markov-chain models for interacting populations whose transition rates are determined by a finite reaction graph. In systems biology they describe random molecule counts in low-copy-number intracellular networks, including signalling and enzymatic systems, gene-regulatory circuits, and synthetic biochemical networks (Anderson and Kurtz, 2015). Such models are often called chemical-master-equation models. For a nonexplosive nonabsorbing irreducible component, a basic stability question is whether it has a stationary probability distribution, or equivalently whether its states have finite mean return times. A stationary law gives a long-run molecule-count distribution and expectations of bounded observables within that component; moments of unbounded count observables require separate integrability. Positive recurrence does not imply that sample paths remain in a bounded set.

The deterministic counterpart supplies additional motivation. Weakly reversible single-linkage mass-action systems are bounded (Anderson, 2011) and permanent (Boros and Hofbauer, 2020) under their deterministic dynamics. Those results express a strong structural stability of concentrations, but deterministic boundedness or permanence does not by itself prove recurrence of the discrete stochastic model. Positive recurrence is the corresponding class-wise stochastic question addressed here.

Anderson and Kim (2018) formulated the positive-recurrence conjecture that weak reversibility should force this stability for stochastic mass-action systems. They established several structural sufficient conditions. Anderson et al. (2020a) subsequently proved the binary, one-linkage case under the additional condition

$$\{S_i, 2S_i\} \cap \mathcal{C} \neq \emptyset \quad \text{for every species } S_i. \quad (1)$$

Thus each species had to occur in a pure unary or pure double complex. The proof of Anderson et al. (2020a) applies an entropy-like function to an n -step embedded chain. In their Section 6, Theorem 6.1 reduces recurrence to their tier inclusion (11): every top S-tier source must also lie in the top D-tier along every proper tier sequence. Lemmas 6.4–6.5 then construct a bounded reaction word and convert its D-tier drop into negative sampled-chain drift. The pure-species assumption enters decisively in the proof of their Theorem 4.1: for a D-top mixed complex $S_u + S_v$ that is disabled because the u -coordinate is zero while the v -coordinate diverges, the existence of S_v or $2S_v$ supplies the comparison needed to establish (11) (Anderson et al., 2020a, Section 6.1, equations (19)–(20), pp. 808–809). The marked-target construction used here avoids that boundary-availability step: the carried target is automatically enabled at the post-jump state, and a directed target-following path propagates its reward until the top-complex alternative supplies a rare terminal source. It therefore does not require a unary or pure-double complex for every species.

Other progress includes complex-balanced product-form systems (Anderson et al., 2010), strongly endotactic structures (Anderson et al., 2020b), one-dimensional classifications (Wiuf and Xu, 2023), a path method for exponential ergodicity (Anderson et al., 2025), and nonexplosion of all second-order weakly reversible systems (Xu, 2026). A complementary two-species positive-recurrence theorem has been publicly announced in conference talks since 2022 (Agazzi, 2022, 2025). The current ConStRAINeD project page lists a five-author proof as in preparation (ConStRAINeD project, 2026). We did not locate a public manuscript for that result as of 9 August 2026. The public descriptions concern two species and permit broader network structure; the present theorem permits arbitrarily many species but assumes one linkage class and molecularity at most two. Neither result should be presented as superseding the other without the announced manuscript. The May 2026 revision of Xu (2026) still records the bimolecular positive-recurrence problem as open.

The present paper removes (1) while retaining the binary and one-linkage assumptions; in particular, its theorem contains the result of Anderson et al. (2020a) as a special case. The exact theorem is stated in Theorem 2.1. It concerns each already-closed communicating class. It does not prove finite expected entrance, from an arbitrary nonclosed initial state, into the union of closed irreducible components. Nor does it address multiple linkage classes or complexes of molecularity above two, and therefore it does not settle the full positive-recurrence conjecture.

A small motivating example is the directed cycle



Species A occurs in neither A nor $2A$, so (1) fails. At the boundary state $(n, 0)$, only the reaction $0 \rightarrow A + B$ is enabled and the one-step drift of total population is positive. The restoring effect

is delayed: the created B enables a fast reaction consuming A . This is representative of why a one-step radial Lyapunov function is not the right universal object.

The delayed correction can be seen directly. Give the three channels in (2) rate constants $\kappa_0, \kappa_1, \kappa_2$, in the order displayed, and begin at the reachable marked state $((n, 0), 0)$. The two designated target-following reactions $0 \rightarrow A + B$ and $A + B \rightarrow B$ each have zero residual-potential increment. The second is selected with probability

$$\frac{\kappa_1(n+1)}{\kappa_0 + \kappa_2 + \kappa_1(n+1)} = 1 - O(n^{-1}).$$

At the resulting marked state $((n, 1), B)$, the expected next increment is

$$-\frac{\kappa_1 n}{\kappa_0 + \kappa_2 + \kappa_1 n} \log n = -\log n + o(\log n). \quad (3)$$

The exceptional branches at the preceding phase have probability $O(n^{-1})$ and increments of order at most $\log n$. Thus the complete target-following episode has a restoring drift of order $-\log n$, even though the first boundary jump increases the total population.

The proof instead uses four ideas. First, we augment the embedded jump chain by marking the actual reaction channel that fired and retaining its target complex. Second, after removing that target from the population, the log-factorial potential has the exact increment

$$\log \frac{(x)_t}{(x)_s}$$

when the carried target is t and the next source is s . Following the carried target therefore costs exactly zero. Third, a finite episode follows a fixed directed path from the carried target toward a selected terminal complex. A sharp scalar envelope shows that a terminal source probability tending to zero forces the complete episode drift to tend to $-\infty$, no matter how the intermediate source rates are separated. Fourth, a normalized-log compactification of an arbitrary divergent sequence gives an exhaustive top-complex case split. Bimolecularity implies either the existence of a higher-weight source enabled over a lower terminal complex or a reaction-wise linear invariant that contradicts divergence inside a fixed communicating class. A finite-family random-time drift argument and a finite trace-chain construction complete the proof.

2 Reaction networks and the stochastic model

Let $\mathcal{S} = \{S_1, \dots, S_d\}$ be a finite species set. A *complex* is a vector $y = (y_1, \dots, y_d) \in \mathbb{N}_0^d$, identified with the formal sum $\sum_i y_i S_i$. Its molecularity is $|y| = \sum_i y_i$. A *reaction channel* is a labelled ordered pair $r : y_r \rightarrow y'_r$, together with a positive rate constant κ_r . Parallel channels are allowed. The reaction graph has the complexes as vertices and the reaction channels as directed edges. Its linkage classes are the connected components of the underlying undirected graph. A network is *weakly reversible* when each linkage class is strongly connected. With one linkage class, weak reversibility is simply strong connectivity of the entire complex graph.

We call the network *binary* or *bimolecular* when

$$|y| \leq 2 \quad \text{for every } y \in \mathcal{C}. \quad (4)$$

Because every complex in a weakly reversible graph is a reaction source, this agrees here with the usual second-order/bimolecular terminology.

For $x \in \mathbb{N}_0^d$, define the multivariate falling factorial

$$(x)_y = \begin{cases} \prod_{i=1}^d \frac{x_i!}{(x_i - y_i)!}, & x \geq y, \\ 0, & \text{otherwise.} \end{cases} \quad (5)$$

The stochastic mass-action propensity of channel r is $\lambda_r(x) = \kappa_r(x)_{y_r}$, and the formal generator is

$$\mathcal{L}f(x) = \sum_r \kappa_r(x)_{y_r} [f(x + y'_r - y_r) - f(x)]. \quad (6)$$

The convention using products of binomial coefficients is equivalent after rescaling each positive rate constant by a fixed factorial factor.

A subset $\Gamma \subseteq \mathbb{N}_0^d$ is a *closed communicating class* when its states communicate through enabled channels and no enabled channel exits Γ . The chain restricted to Γ is irreducible. In a nonabsorbing class, let J_1 be the first jump time and define the positive return time to x by $T_x^+ = \inf\{t \geq J_1 : X(t) = x\}$. The class is *positive recurrent* when one, equivalently every, state has $\mathbb{E}_x T_x^+ < \infty$. Absorbing singleton classes are handled separately: their stationary probability is the point mass at the absorbing state. Henceforth positive return times are discussed only for nonabsorbing irreducible classes. For a nonexplosive irreducible countable-state CTMC, positive recurrence is equivalent to the existence of a stationary probability distribution (Norris, 1997).

A channel $y \rightarrow y$ has zero population increment and contributes zero to (6); discard it. Exact parallel channels with the same source and target may be combined by adding their rates. Channels having the same population displacement but different sources or targets remain distinct, because the proof marks the actual channel. All reaction-indexed sums and rate quantities below, including Λ and $\bar{\kappa}_y$, refer to this reduced set of genuine channels.

Every finite nonabsorbing closed communicating class is positive recurrent: its finite irreducible jump chain has a stationary probability distribution, all state rates are finite, and the associated finite-state CTMC is nonexplosive (Norris, 1997). If the complex graph has one vertex, all closed classes are absorbing singletons. If all complexes have the same molecularity, every reaction preserves $|x|_1$, so each communicating class lies in a finite shell. We therefore fix henceforth an infinite closed irreducible class Γ , a strongly connected graph with at least two complexes, and no self channels. Every complex then has a genuine outgoing channel. Write

$$\bar{\kappa}_y = \sum_{r: y_r=y} \kappa_r, \quad \bar{\kappa}_- = \min_{y \in \mathcal{C}} \bar{\kappa}_y > 0, \quad \bar{\kappa}_+ = \max_{y \in \mathcal{C}} \bar{\kappa}_y. \quad (7)$$

Theorem 2.1 (Binary one-linkage positive recurrence). *Let a finite stochastic mass-action reaction network be weakly reversible, have one linkage class, and satisfy (4). For every positive rate vector, the minimal population CTMC restricted to each closed communicating class is nonexplosive. Every nonabsorbing such class is positive recurrent; each absorbing singleton has its point-mass stationary law.*

Corollary 2.2 (Stationary probability). *Under the hypotheses of Theorem 2.1, every closed communicating class Γ admits a stationary probability distribution π_Γ . It is unique on Γ .*

3 The marked target-augmented chain

We first define the embedded chain without assuming nonexplosion. At a nonabsorbing population state x , sample the actual labelled reaction channel r with probability

$$\frac{\kappa_r(x)_{y_r}}{\Lambda(x)}, \quad \Lambda(x) = \sum_q \kappa_q(x)_{y_q}. \quad (8)$$

This discrete chain can be constructed independently of its holding times. After the sampled channel r fires, record its target $t = y'_r$. The mark is therefore obtained from the actual channel and is never inferred from the population displacement. Once exact parallel channels with the same source and target have been aggregated, retaining the target is the only part of the previous channel needed below. Write Z_n for this target-augmented embedded chain. A reachable augmented state is denoted (x, t) , where x is the post-jump population. If the next sampled channel is $q : s \rightarrow u$, then

$$(x, t) \mapsto (x - s + u, u). \quad (9)$$

The channel law depends on x , not on the historical mark, so the augmented process is Markov, and projection onto x is the ordinary population embedded chain.

Let $\tilde{\Gamma}$ be the augmented states reachable after genuine jumps within Γ . It is closed under (9). It is also irreducible, and its projection onto the population coordinate is exactly Γ . For the latter assertion, every $x \in \Gamma$ terminates a positive-length population path: irreducibility gives such a path directly, or, if necessary, one may take a genuine outgoing jump and a return path. The final channel supplies a reachable mark over x . For irreducibility, given $(x, t), (x', t') \in \tilde{\Gamma}$, choose a channel $s' \rightarrow t'$ and predecessor population $z = x' - t' + s' \in \Gamma$ witnessing reachability of the second pair. Population irreducibility supplies a positive-probability marked-channel path from x to z ; appending $s' \rightarrow t'$ reaches (x', t') .

The carried target is always enabled. If the preceding channel was $s \rightarrow t$, then its post-jump state has the form $x = z - s + t \geq t$. Put

$$r = x - t \in \mathbb{N}_0^d, \quad V(x, t) = \sum_{i=1}^d \log((x_i - t_i)!) = \sum_i \log(r_i!). \quad (10)$$

We use $\log(0!) = 0$. Thus $V \geq 0$. Every sublevel set of V in $\tilde{\Gamma}$ is finite, because $\log(n!) \rightarrow \infty$, each residual coordinate is bounded on a sublevel, and the target set is finite.

The entropy growth in (10) is classical. With $0 \log 0 = 0$, Stirling's formula gives

$$\sum_i \log(r_i!) = \sum_i (r_i \log r_i - r_i) + O\left(\sum_i \log(r_i + 1)\right). \quad (11)$$

This leading term is in the pseudo-Helmholtz or Horn–Jackson family

$$G_c(r) = \sum_i [r_i (\log(r_i/c_i) - 1) + c_i], \quad c_i > 0,$$

used in deterministic and stochastic chemical reaction network theory (Horn and Jackson, 1972; Anderson et al., 2015). Thus the residual log-factorial potential is a discrete, target-shifted analogue of that classical entropy, not the Horn–Jackson function itself. The target shift is the new feature in this argument: subtracting the complex actually produced by the preceding channel gives the exact identity below, rather than only an asymptotic Lyapunov estimate, and makes every target-following jump have exactly zero increment.

Lemma 3.1 (Exact target/source identity). *At (x, t) , if the next marked channel has source s and target u , then*

$$V(x - s + u, u) - V(x, t) = \log \frac{(x)_t}{(x)_s}. \quad (12)$$

In particular, a channel sourced at the carried target has zero increment.

Proof. The new residual is $(x - s + u) - u = x - s$. Since both s and t are enabled,

$$\exp(\Delta V) = \prod_i \frac{(x_i - s_i)!}{(x_i - t_i)!} = \frac{(x)_t}{(x)_s}.$$

□

This identity gives a precise “complete-credit” interpretation: a product complex remains credited in full until the chain chooses a different source. The interpretation is not used in place of the algebraic identity.

For enabled source complexes define

$$p_x(y) = \frac{\bar{\kappa}_y(x)_y}{\Lambda(x)}. \quad (13)$$

Set $p_x(y) = 0$ for disabled sources, and use $0 \log 0 = 0$ in entropy expressions. Unless explicitly stated otherwise, sums in this subsection range only over enabled source complexes. Because the carried target is enabled, $p_x(t) > 0$. The expected one-jump increment is

$$d(x, t) = \sum_{s: x \geq s} p_x(s) \log \frac{(x)_t}{(x)_s}. \quad (14)$$

Lemma 3.2 (Source-probability bound). *For every reachable augmented state,*

$$\begin{aligned} d(x, t) &= \log p_x(t) - \sum_{s: x \geq s} p_x(s) \log p_x(s) \\ &\quad + \sum_{s: x \geq s} p_x(s) \log \bar{\kappa}_s - \log \bar{\kappa}_t, \end{aligned} \quad (15)$$

and consequently

$$d(x, t) \leq \log p_x(t) + C_0, \quad C_0 = \log |\mathcal{C}| + \log \frac{\bar{\kappa}_+}{\bar{\kappa}_-}. \quad (16)$$

Proof. For each enabled s , $(x)_s = p_x(s) \Lambda(x) / \bar{\kappa}_s$. Substitution into (14) gives (15). The entropy of a probability vector supported on at most $|\mathcal{C}|$ points is at most $\log |\mathcal{C}|$, and the last line contributes at most $\log(\bar{\kappa}_+ / \bar{\kappa}_-)$. The zero complex creates no exception, since $(x)_0 = 1$. □

4 Propagation along target-following paths

For every ordered pair $(t, c) \in \mathcal{C}^2$, fix a simple directed path of marked channels

$$t = y_0 \longrightarrow y_1 \longrightarrow \cdots \longrightarrow y_L = c, \quad 0 \leq L \leq |\mathcal{C}| - 1. \quad (17)$$

Strong connectivity supplies the path. Starting from $(r + t, t)$, define the (t, c) -episode as follows. At phase y_k , $k < L$, continue only when the exact designated channel $y_k \rightarrow y_{k+1}$ fires; after any

other channel, stop immediately. If the path reaches c , take one final ordinary jump and stop. When $c = t$, the path has length zero and the episode is just that final jump.

This is a stopping time for the marked embedded filtration. On designated edges the lifted populations are

$$r + y_0 \longrightarrow r + y_1 \longrightarrow \cdots \longrightarrow r + c. \quad (18)$$

Every designated source is literally present, the residual remains r , and closedness of Γ keeps the entire lift in the class. The episode has between one and $|\mathcal{C}|$ jumps and only finitely many terminal branches.

For the designated channel at phase k , put

$$q_k = \frac{\kappa_{y_k \rightarrow y_{k+1}}}{\bar{\kappa}_{y_k}} > 0, \quad p_k = p_{r+y_k}(y_k). \quad (19)$$

Let $J_k(r)$ be the expected remaining V -increment from phase k .

Lemma 4.1 (Exact episode recursion). *The episode rewards satisfy*

$$J_L(r) = d(r + c, c), \quad J_k(r) = d(r + y_k, y_k) + q_k p_k J_{k+1}(r). \quad (20)$$

Proof. At phase k , the first jump has expected increment $d(r + y_k, y_k)$. Continuation occurs exactly when the designated channel fires, with probability $q_k p_k$. That channel is sourced at the carried target and has zero immediate increment by Lemma 3.1; the remaining conditional expectation is $J_{k+1}(r)$. $\square$

The following scalar calculation controls all possible intermediate source probabilities.

Lemma 4.2 (Scalar envelope). *For $q > 0$ and $M \in \mathbb{R}$, define*

$$F_q(M) = \sup_{0 < p \leq 1} \{\log p + C_0 + qpM\}.$$

The function F_q is nondecreasing in M . Then

$$F_q(M) = \begin{cases} C_0 + qM, & M \geq -1/q, \\ C_0 - 1 - \log(-qM), & M < -1/q. \end{cases} \quad (21)$$

Consequently, if $M_n \rightarrow -\infty$, then $F_q(M_n) \rightarrow -\infty$.

Proof. For each fixed $p \in (0, 1]$, the displayed objective is increasing in M , with slope $qp > 0$; taking its supremum proves monotonicity. The objective has derivative $p^{-1} + qM$ and second derivative $-p^{-2} < 0$. If $M \geq -1/q$, its derivative at $p = 1$ is nonnegative, so concavity places the maximum at $p = 1$. If $M < -1/q$, the unique maximizer is $p = (-qM)^{-1} \in (0, 1)$, which gives the second line of (21). The final assertion follows immediately. $\square$

Proposition 4.3 (Propagation of terminal drift). *Fix a target-following path (17). If along a sequence of residuals $r^{(n)}$ one has*

$$p_{r^{(n)}+c}(c) \longrightarrow 0,$$

then the expected increment of the complete (t, c) -episode tends to $-\infty$.

Proof. At the terminal phase, Lemma 3.2 gives $J_L \leq \log p_{r+c}(c) + C_0 \rightarrow -\infty$. If $J_{k+1} \leq M$, then the monotonicity just proved and Lemmas 3.2 and 4.1 give

$$J_k \leq \sup_{0 < p \leq 1} \{\log p + C_0 + q_k p M\} = F_{q_k}(M).$$

Apply Lemma 4.2 backward through the finite path. $\square$

The proof preserves every reaction-rate monomial: no edge is replaced and no unrelated rates are compared. Arbitrarily many nested source-rate scales are absorbed by the finite scalar recursion.

5 Logarithmic compactification and the top-complex alternative

We now show that every divergent augmented sequence supplies the terminal rarity required by Proposition 4.3, unless a linear stoichiometric invariant already makes such divergence impossible.

Take a sequence $(x^{(n)}, t^{(n)}) \in \tilde{\Gamma}$ leaving every finite set. Pass to a subsequence with $t^{(n)} = t$, and set $r^{(n)} = x^{(n)} - t$. A diagonal extraction makes every coordinate of $r^{(n)}$ either one fixed nonnegative integer or divergent to infinity. Let I be the set of divergent coordinates and put

$$R_n = \sum_{i \in I} \log(r_i^{(n)} + 1). \quad (22)$$

After a further subsequence, the limits

$$w_i = \lim_{n \rightarrow \infty} \frac{\log(r_i^{(n)} + 1)}{R_n} \quad (i \in I), \quad w_i = 0 \quad (i \notin I) \quad (23)$$

exist. Thus $w \geq 0$ and $\sum_i w_i = 1$.

Remark 5.1 (Slower divergent tiers). A coordinate can diverge while having $w_i = 0$. It remains in I : zero normalized logarithmic weight means growth on a slower divergent tier, not a bounded species. This distinction is essential in the availability and signed-invariant branches of Lemma 5.3.

Lemma 5.2 (Falling-factorial asymptotics). *Let c and y be fixed complexes, and suppose y is enabled at $r^{(n)} + c$ for all sufficiently large n . Then*

$$\log(r^{(n)} + c)_y = R_n w \cdot y + o(R_n). \quad (24)$$

Proof. For $y_i = 1$ and a divergent coordinate, $\log(r_i^{(n)} + c_i) = \log(r_i^{(n)} + 1) + o(R_n)$; a fixed coordinate contributes $O(1)$. For $y_i = 2$ and $r_i^{(n)} \rightarrow \infty$,

$$\log((r_i^{(n)} + c_i)(r_i^{(n)} + c_i - 1)) = 2\log(r_i^{(n)} + 1) + o(R_n).$$

If that coordinate is fixed, enabledness makes its contribution finite and hence $O(1)$. Summing the coordinate contributions proves the claim. $\square$

For a complex y , write $h(y) = w \cdot y$, and define

$$a = \max_{y \in \mathcal{C}} h(y), \quad T = \{y \in \mathcal{C} : h(y) = a\}. \quad (25)$$

The next lemma contains the decisive use of bimolecularity. When $T \neq \mathcal{C}$, its maximal weight satisfies $a > 0$, so every top complex contains at least one particle in a divergent coordinate. Because a binary complex contains at most two particles, only two configurations remain: a top complex contains two such particles, or every top complex contains exactly one. This elementary restriction makes the following alternative exhaustive; it is precisely what fails without the molecularity bound.

Lemma 5.3 (Top-complex availability or invariant). *Along the divergent sequence, at least one of the following conclusions is available:*

- (i) *a reaction-wise linear stoichiometric invariant has value tending to infinity along the sequence, contradicting membership in the fixed communicating class; or*
- (ii) *there are fixed complexes $s, c \in \mathcal{C}$ with $h(s) > h(c)$ such that both s and c are enabled at $r^{(n)} + c$ for all sufficiently large n .*

Proof. We follow the three exhaustive cases described above. First, if every complex is top, then $w \cdot (y' - y) = 0$ for every channel. Therefore $w \cdot X$ is a nonnegative linear invariant. A coordinate with positive weight diverges, so the invariant value tends to infinity, which is impossible inside one communicating class.

Second, assume $T \neq \mathcal{C}$ and a top complex s contains two particles supported on coordinates in I . Bimolecularity forces s to contain no particle supported on a bounded coordinate. Both required particles are eventually present in $r^{(n)}$, including the case $s = 2S_i$. Hence s is enabled at $r^{(n)} + c$ for every lower $c \notin T$, and $h(s) > h(c)$.

Third, suppose every top complex contains exactly one particle supported on a coordinate in I . Let $J \subseteq I$ be the species appearing in top complexes. If $i \in J$, the remaining possible particle in that top complex is supported on a bounded coordinate and therefore has weight zero; consequently $w_i = a$. No complex contains two J -particles, since its weight would be at least $2a > a$. Moreover,

$$y \in T \iff q_J(y) := \sum_{i \in J} y_i = 1. \quad (26)$$

The forward implication follows from the definition of J . Conversely, one J -particle already contributes a ; maximality forces all other weight to be zero and makes the complex top.

If every complex had $q_J = 1$, then (26) would give $T = \mathcal{C}$, the all-top case already handled above. There remain three subcases.

- (a) If a unary top complex S_i , $i \in J$, exists, it is enabled over every lower terminal complex, giving conclusion (ii).
- (b) Otherwise every top complex has the form $S_i + D$, where $D \notin I$; call D a bounded companion species. If a lower complex c contains such a D , the corresponding top source $S_i + D$ is enabled at $r^{(n)} + c$, giving conclusion (ii).
- (c) If no lower complex contains any bounded companion species, let $\mathcal{D}$ be the set of distinct companion species. The signed linear functional

$$\ell(x) := \sum_{i \in J} x_i - \sum_{D \in \mathcal{D}} x_D \quad (27)$$

has value zero on every complex: each top complex contains one J -particle and one companion particle, whereas a lower complex contains neither. It is therefore reaction-wise invariant. Its positive part diverges, while every companion coordinate lies outside I and is fixed along the subsequence. Its value tends to infinity, contradicting the fixed communicating class.

This exhausts all binary complexes. We reserve “conservation law” for the nonnegative invariants above; (27) is a signed linear stoichiometric invariant. $\square$

The invariant contradiction is exact: if $\ell \cdot (y' - y) = 0$ on every channel, then $\ell \cdot x$ is constant along every path in Γ . In the signed branch, the coordinates with negative coefficients are fixed

along the extracted sequence, so the invariant really does tend to $+\infty$. A species absent from every complex is itself reaction-wise invariant; thus an absent coordinate cannot diverge along a fixed communicating class.

Lemma 5.4 (Vanishing terminal source probability). *Under conclusion (ii) of Lemma 5.3,*

$$p_{r^{(n)}+c}(c) \longrightarrow 0. \quad (28)$$

Proof. Both s and c are enabled. Lemma 5.2 and the strict gap $h(s) > h(c)$ give

$$\frac{(r^{(n)} + c)_s}{(r^{(n)} + c)_c} \longrightarrow \infty.$$

Consequently,

$$p_{r^{(n)}+c}(c) \leq \frac{\bar{\kappa}_c(r^{(n)} + c)_c}{\bar{\kappa}_s(r^{(n)} + c)_s} \longrightarrow 0.$$

□

6 Uniform random-time drift outside a finite set

For each $c \in \mathcal{C}$, let $D_c(x, t)$ denote the exact expected increment of the fixed (t, c) -episode. Define

$$K = \left\{ (x, t) \in \tilde{\Gamma} : \min_{c \in \mathcal{C}} D_c(x, t) > -1 \right\}. \quad (29)$$

Proposition 6.1 (Finite and nonempty exceptional set). *The set K is finite and nonempty.*

Proof. Suppose first that K were infinite. Properness of V supplies a sequence in K leaving every finite set. Apply the compactification of Section 5. An invariant conclusion from Lemma 5.3 contradicts membership in one communicating class. Otherwise, Lemma 5.4 and Proposition 4.3 supply a fixed terminal complex c for which $D_c(x^{(n)}, t) \rightarrow -\infty$. This contradicts the definition of K . Thus K is finite.

To prove nonemptiness, select any augmented state z_0 . The finite nonempty sublevel set $\{z : V(z) \leq V(z_0)\}$ contains a global minimizer z_* of V . Every endpoint of every target-following episode remains in $\tilde{\Gamma}$, so its potential is at least $V(z_*)$. Hence $D_c(z_*) \geq 0$ for every c , and $z_* \in K$. □

Remark 6.2 (Rate dependence of the exceptional set). The finiteness proof is qualitative and cannot give a rate-independent bound on the location of K . Consider the directed cycle

$$0 \xrightarrow{\kappa_0} A \xrightarrow{\kappa_1} A + B \xrightarrow{\kappa_2} 0$$

and the augmented state $((m, 0), A)$, $m \geq 2$. The population chain is irreducible on $\mathbb{N}_0^2$, and each such marked state is reachable after a $0 \rightarrow A$ jump from $(m - 1, 0)$; hence all these states lie in one fixed augmented class. For the target-following path from A through $A + B$ to terminal 0, the exact recursion gives

$$D_0(m, A) = a_m + p_m(b_m + q_m c_m), \quad (30)$$

where

$$\begin{aligned} a_m &= \frac{\kappa_0 \log m}{\kappa_0 + \kappa_1 m}, & p_m &= \frac{\kappa_1 m}{\kappa_0 + \kappa_1 m}, \\ b_m &= \frac{\kappa_0 \log m}{\kappa_0 + (\kappa_1 + \kappa_2)m}, & q_m &= \frac{\kappa_2 m}{\kappa_0 + (\kappa_1 + \kappa_2)m}, \\ c_m &= -\frac{\kappa_1(m - 1)}{\kappa_0 + \kappa_1(m - 1)} \log(m - 1). \end{aligned}$$

The three terms are respectively the drift at carried targets A , $A + B$, and 0, with p_m and q_m the exact continuation probabilities. Hence

$$D_0(m, A) = -\frac{\kappa_2}{\kappa_1 + \kappa_2} \log m + O\left(\frac{\log m}{m}\right). \quad (31)$$

For the other two possible terminals, the same path library gives $D_A(m, A) = a_m > 0$ and $D_{A+B}(m, A) = a_m + p_m b_m > 0$. With κ_0, κ_1 fixed, (30) tends to $a_m + p_m b_m > 0$ as $\kappa_2 \downarrow 0$ for each fixed m . Thus, for every finite M , a sufficiently small positive κ_2 puts all the states $((m, 0), A)$, $2 \leq m \leq M$, in K . At the same time the negative coefficient in (31) can be arbitrarily small. Consequently, neither the location nor the diameter of K is bounded by the numbers of species and complexes alone, uniformly over positive rate vectors.

Outside K , choose the lexicographically first terminal complex minimizing $D_c(x, t)$, before the episode begins. This is a deterministic measurable selector on the countable state space and is compatible with restarting under the strong Markov property. Its episode stopping time τ obeys

$$1 \leq \tau \leq L := |\mathcal{C}|, \quad \mathbb{E}_{(x,t)}[V(Z_\tau) - V(x, t)] \leq -1, \quad (x, t) \notin K. \quad (32)$$

The coordinate overshoot in one episode is deterministically bounded by $2L$, because each binary reaction changes each population coordinate by at most two.

7 Positive recurrence

The following argument is a short specialization of standard sampled-chain Foster theory (Meyn and Tweedie, 2009); we include it to record the exact stopping and return interfaces used here.

Let $Y_0 = z$. If $Y_n \notin K$, let Y_{n+1} be the endpoint of the episode selected at Y_n ; if $Y_n \in K$, set $Y_{n+1} = Y_n$. Thus the endpoint chain is stopped upon entering K . Put $\sigma_K = \inf\{n \geq 0 : Y_n \in K\}$. Let $\mathcal{G}_n$ be the endpoint-chain filtration and define

$$W_n = V(Y_{n \wedge \sigma_K}) + (n \wedge \sigma_K).$$

The drift bound (32) makes (W_n) a nonnegative supermartingale. Its terms are integrable: after at most N episodes, each population coordinate is bounded above by its initial value plus $2LN$, by the deterministic overshoot bound following (32); the finite target set then bounds V . Applying the supermartingale inequality at the bounded time N gives

$$\mathbb{E}_z V(Y_{N \wedge \sigma_K}) + \mathbb{E}_z (N \wedge \sigma_K) \leq V(z). \quad (33)$$

Because $V \geq 0$, expectations and monotone convergence yield

$$\mathbb{E}_z \sigma_K \leq V(z). \quad (34)$$

The original augmented embedded chain therefore hits K in finite expected jump count, bounded by $LV(z)$.

The following finite trace argument turns hitting K into positive return to one state; the finite-chain step is standard (Norris, 1997), while the conversion from trace excursions to original jumps is recorded explicitly.

Proposition 7.1 (Finite trace-chain closure). *The augmented embedded chain has a state with finite expected positive return time.*

Proof. Let $T_K^+ = \inf\{n \geq 1 : Z_n \in K\}$. From $k \in K$, take one ordinary jump. There are finitely many channel successors, and from each successor the expected hitting time of K is finite by (34). Thus $\mathbb{E}_k T_K^+ < \infty$ for every $k \in K$.

Record successive visits to K . The resulting trace chain is finite and irreducible. Indeed, any augmented path between two points of K , with its intermediate K -visits retained, gives a positive-probability trace path. Fix $k_* \in K$. From every trace state choose a finite positive-probability trace path to k_* . Finiteness supplies common constants $m < \infty$ and $\varepsilon > 0$ such that, from every trace state, k_* is hit within the next m trace transitions with probability at least ε . Starting from k_* , first take one trace transition and then apply this estimate in successive blocks of m transitions. The number of blocks before the next visit to k_* is geometrically dominated, so the positive trace return time has finite mean.

Finally, set

$$B = \max_{k \in K} \mathbb{E}_k T_K^+ < \infty.$$

If M is the positive trace return count and L_j is the number of original jumps in its j -th trace excursion, let $\mathcal{F}_j$ be the sigma-field at the start of that excursion. Continue the trace chain after its return to k_* , so these objects are defined for all $j \geq 0$. Then $\{j < M\} \in \mathcal{F}_j$, and the strong Markov property gives $\mathbb{E}[L_j \mid \mathcal{F}_j] \leq B$. Tonelli's theorem and the tail-sum formula therefore yield

$$\begin{aligned} \mathbb{E} \left[\sum_{j=0}^{M-1} L_j \right] &= \sum_{j \geq 0} \mathbb{E} [\mathbf{1}_{\{j < M\}} L_j] \\ &\leq B \sum_{j \geq 0} \mathbb{P}(j < M) = B \mathbb{E} M < \infty. \end{aligned}$$

Hence the augmented embedded chain has finite expected positive return time to k_* . $\square$

Projection away from the target mark shows that the population embedded chain has finite expected positive return to the population coordinate x_* of k_* : its first positive population return occurs no later than the marked return to k_* . It remains to construct physical time and rule out explosion.

Proposition 7.2 (Embedded-chain-to-CTMC conversion). *Let a countable irreducible embedded chain be positive recurrent. Suppose a pure-jump construction assigns a finite rate $\Lambda(x) > 0$ at every state and that $\inf_x \Lambda(x) > 0$. Then the resulting minimal CTMC is nonexplosive and positive recurrent.*

Proof. Let N be a finite-mean positive return count to a recurrent embedded state x_* , and let H_j be the holding times. Conditional on the embedded path, H_j is exponential with mean $1/\Lambda(X_j)$. Tonelli's theorem and conditional expectation give

$$\mathbb{E} \sum_{j=0}^{N-1} H_j = \mathbb{E} \sum_{j \geq 0} \mathbf{1}_{\{j < N\}} \frac{1}{\Lambda(X_j)} \leq \frac{\mathbb{E} N}{\inf_x \Lambda(x)} < \infty.$$

Thus the expected physical return time is finite, provided the construction is nonexplosive.

Finite mean return makes x_* recurrent for the embedded chain, so it is visited infinitely often almost surely. On each visit, the following holding time has the same exponential law of finite rate $\Lambda(x_*)$. The strong Markov construction makes these recurrent holding times independent copies. Their infinite sum diverges almost surely. Since total physical time dominates this subseries, jump times cannot accumulate at a finite time. The minimal CTMC is nonexplosive and has finite mean positive return time to x_* . $\square$

Apply Proposition 7.2 directly to the population embedded chain on Γ . Let $\kappa_{\min} = \min_r \kappa_r > 0$, with the minimum taken over the finite reduced set of genuine channels. Every $x \in \Gamma$ enables at least one such channel r ; otherwise x would be absorbing and the infinite irreducible class Γ would be a singleton. Since a positive falling factorial is an integer,

$$\Lambda(x) \geq \kappa_r(x)_{y_r} \geq \kappa_{\min}, \quad x \in \Gamma. \quad (35)$$

Propositions 7.1 and 7.2 therefore prove Theorem 2.1. For context, nonexplosion was previously obtained for complex-balanced stochastic systems through a stationary-integrability argument (Anderson et al., 2018). For the present subclass, the return-cycle construction recovers nonexplosion directly, consistently with the more general second-order endotactic nonexplosion theorem of Xu (2026).

The same return cycle yields Corollary 2.2. Explicitly, for the positive return time $T_{x_*}^+$ defined in Section 2,

$$\pi_\Gamma(y) = \frac{\mathbb{E}_{x_*} \left[\int_0^{T_{x_*}^+} \mathbf{1}_{\{X(t)=y\}} dt \right]}{\mathbb{E}_{x_*} T_{x_*}^+}, \quad y \in \Gamma, \quad (36)$$

is the normalized mean occupation measure of one regenerative cycle. The standard regenerative occupation theorem makes this measure stationary (Asmussen, 2003); its denominator normalizes it to one, and irreducibility gives uniqueness.

8 Scope and further questions

The proof is class-wise. Coordinate faces, siphons, parity restrictions, and other lattice constraints require no separate interior argument: every constructed target-following path consists of actual enabled channels and therefore remains in the fixed closed class. Species absent from all complexes are constant on each class and appear automatically in the invariant branch of Lemma 5.3.

Three stability statements should be distinguished. Theorem 2.1 proves positive recurrence on every communicating class that is already closed. It does not prove the additional Anderson–Kim stability property of finite expected entrance, from an arbitrary initial state, into the union of closed irreducible components. The larger questions of multiple linkage classes, molecularity above two, and the full weakly reversible stochastic positive-recurrence conjecture also remain open.

The one-linkage hypothesis is used at one decisive point: for every carried target t and selected terminal complex c , a directed path (17) must exist. With several linkage classes, a carried target need not reach a terminal source belonging to another class, so the finite path library does not directly glue. That extension remains open here.

Bimolecularity is used in the exhaustive case split of Lemma 5.3: a top complex either contains two particles supported on divergent coordinates or exactly one such particle, leaving at most one bounded companion species. Complexes of molecularity three or higher admit additional top configurations not covered by the argument. No claim is made for them.

The potentially reusable part of the proof is the combination of marked reaction-channel augmentation, subtraction of the carried target, the exact residual-factorial increment, finite target-following propagation, and normalized-log top-complex compactification. The multiple-linkage obstruction is precise: a target in one linkage class need not have a directed path to a useful terminal complex in another linkage class. Overcoming that obstruction would require an additional mechanism and is not a routine extension of the present path argument.

The proof establishes positive recurrence and the existence of a stationary probability distribution. It does not provide a product form, explicit tail bounds, exponential ergodicity, or quantitative mixing rates. The finite set K is obtained by analytic compactness, not by enumeration, and the proof gives no practically useful universal estimate of its location or diameter. Its scale can depend arbitrarily strongly on positive rate ratios, as the exact example following Proposition 6.1 illustrates. Effective rate-dependent recurrence, tail, and mixing estimates remain open.

Relevance to stochastic systems biology

Chemical-master-equation models represent molecule-count noise in low-copy-number biochemical networks. When a model satisfies weak reversibility, one linkage class, and bimolecularity, the theorem supplies a parameter-independent structural conclusion: for every choice of positive rate constants, each closed communicating class has one stationary probability law. Within such a class, the long-run molecule-count distribution, state frequencies, and stationary averages of bounded observables are therefore defined, and the process cannot escape permanently to infinity. Means, correlations, and other moments of unbounded count observables are available only when they are integrable under that law.

The hypotheses are structural restrictions, not claims about all biological networks. The conclusion provides neither an explicit stationary formula nor a mixing-time estimate, and it does not say that individual sample paths stay inside a bounded region. Large transient excursions remain possible, with no quantitative bound supplied here. The result is thus a qualitative stability criterion for those intracellular, signalling, enzymatic, gene-regulatory, or synthetic biochemical models whose effective reaction graphs fall within the stated class; no empirical or organism-specific validation is asserted.

Declarations

Author information. Alec Kriebel, Independent researcher.

Correspondence: me@aleckriebel.com.

ORCID: 0009-0001-9320-500X.

Code availability. The self-contained verification package and supporting materials are available in the public project repository at https://github.com/AlecKriebel/Math/tree/bimolecular-positive-recurrence-v1.0/bimolecular_positive_recurrence_publication_v1. The submitted archive is also supplied with the manuscript so that its exact Git snapshot and checksums can be retained with the submission record. No computation is used in the universal proof.

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A Technical details for the trace chain and physical time

This appendix records several interfaces that can otherwise be obscured by standard Markov-chain shorthand.

First, the augmented state records the actual marked channel. If two channels have the same population displacement but different sources or targets, their post-jump populations can agree while their carried targets do not. They therefore remain separate. Only channels with identical source and target may be aggregated.

Second, K in (29) is nonempty, not merely finite. The global minimum argument in Proposition 6.1 is pathwise: every possible episode endpoint has potential at least the starting minimum. No optional stopping or integrability assertion is needed for this step because each episode has at most $|\mathcal{C}|$ jumps.

Third, the trace-chain proof distinguishes hitting from return. The first ordinary jump from $k \in K$ forces a positive return time. The finite expected time back to K follows by conditioning on finitely many successors. The subsequent geometric-block argument is applied to the finite trace chain, and only afterward are the random trace excursions expanded into original embedded jumps.

Fourth, the embedded chain is constructed first. Its recurrent population state x_* is visited infinitely often. The holding times attached to those visits form an infinite sequence of independent exponentials with one fixed finite rate, whose sum diverges almost surely. This directly prevents finite-time accumulation.

Finally, singleton absorbing classes are handled before augmentation. In an infinite irreducible class every population state has an enabled genuine channel; otherwise it would be absorbing and its class would be a singleton.

B Supplementary computational checks

The accompanying dependency-free Python package performs exact-arithmetic checks of the falling-factorial identity and entropy rewrite, verifies the scalar-envelope branch conditions, and tests the top-complex classification on a deterministic finite atlas with separately validated witnesses. It also contains fixed-seed falsification tests and exact finite calibrations of the rate-degeneration example and stationary return-cycle formula. No finite atlas or random test proves the universal theorem,

and simulations do not prove recurrence. In particular, the finiteness of K follows only from the analytic compactness proof: the package neither enumerates K nor certifies a practical upper bound on its size, diameter, or location.

References

- Andrea Agazzi. Weakly reversible chemical reaction networks are recurrent in 2d. Talk at the Jean-Pierre Eckmann 75 Conference, University of Geneva, 2022. URL <https://www.unige.ch/jpe75conference/program.html>. Public program dated 10 June 2022; joint work with Jonathan C. Mattingly, David F. Anderson, and Daniele Cappelletti.
- Andrea Agazzi. Weakly reversible chemical reaction networks are recurrent in 2d. Talk abstract, SIAM Conference on Applied Algebraic Geometry (AG25), 2025. URL https://www.siam.org/media/13rgukxr/ag25_abstracts.pdf. Official abstract book, p. 79; conference held 7–11 July 2025.
- David F. Anderson. Boundedness of trajectories for weakly reversible, single linkage class reaction systems. *Journal of Mathematical Chemistry*, 49(10):2275–2290, 2011. doi: 10.1007/s10910-011-9886-4.
- David F. Anderson and Jinsu Kim. Some network conditions for positive recurrence of stochastically modeled reaction networks. *SIAM Journal on Applied Mathematics*, 78(5):2692–2713, 2018. doi: 10.1137/17M1161427.
- David F. Anderson and Thomas G. Kurtz. *Stochastic Analysis of Biochemical Systems*, volume 1 of *Mathematical Biosciences Institute Lecture Series*. Springer, Cham, 2015. doi: 10.1007/978-3-319-16895-1.
- David F. Anderson, Gheorghe Craciun, and Thomas G. Kurtz. Product-form stationary distributions for deficiency zero chemical reaction networks. *Bulletin of Mathematical Biology*, 72(8):1947–1970, 2010. doi: 10.1007/s11538-010-9517-4.
- David F. Anderson, Gheorghe Craciun, Manoj Gopalkrishnan, and Carsten Wiuf. Lyapunov functions, stationary distributions, and non-equilibrium potential for reaction networks. *Bulletin of Mathematical Biology*, 77(9):1744–1767, 2015. doi: 10.1007/s11538-015-0102-8.
- David F. Anderson, Daniele Cappelletti, Masanori Koyama, and Thomas G. Kurtz. Non-explosivity of stochastically modeled reaction networks that are complex balanced. *Bulletin of Mathematical Biology*, 80(10):2561–2579, 2018. doi: 10.1007/s11538-018-0473-8.
- David F. Anderson, Daniele Cappelletti, and Jinsu Kim. Stochastically modeled weakly reversible reaction networks with a single linkage class. *Journal of Applied Probability*, 57(3):792–810, 2020a. doi: 10.1017/jpr.2020.28.
- David F. Anderson, Daniele Cappelletti, Jinsu Kim, and Tung D. Nguyen. Tier structure of strongly endotactic reaction networks. *Stochastic Processes and their Applications*, 130(12):7218–7259, 2020b. doi: 10.1016/j.spa.2020.07.012.
- David F. Anderson, Daniele Cappelletti, Wai-Tong Louis Fan, and Jinsu Kim. A new path method for exponential ergodicity of markov processes on $\mathbb{Z}^d$, with applications to stochastic reaction

- networks. *SIAM Journal on Applied Dynamical Systems*, 24(2):1668–1710, 2025. doi: 10.1137/24M1665933.
- Søren Asmussen. *Applied Probability and Queues*, volume 51 of *Stochastic Modelling and Applied Probability*. Springer, New York, 2 edition, 2003. ISBN 978-0-387-00211-8. doi: 10.1007/b97236.
- Balázs Boros and Josef Hofbauer. Permanence of weakly reversible mass-action systems with a single linkage class. *SIAM Journal on Applied Dynamical Systems*, 19(1):352–365, 2020. doi: 10.1137/19M1248431.
- ConStRAINeD project. Results and publications. PRIN 2022 project website, 2026. URL <https://constrained.polito.it/publications/>. Accessed 9 August 2026; year is the access year; item 16 lists the two-dimensional chemical recurrence proof as in preparation.
- Friedrich J. M. Horn and Roy Jackson. General mass action kinetics. *Archive for Rational Mechanics and Analysis*, 47(2):81–116, 1972. doi: 10.1007/BF00251225.
- Sean P. Meyn and Richard L. Tweedie. *Markov Chains and Stochastic Stability*. Cambridge University Press, 2 edition, 2009. ISBN 978-0-521-73182-9. doi: 10.1017/CBO9780511626630.
- J. R. Norris. *Markov Chains*. Number 2 in Cambridge Series in Statistical and Probabilistic Mathematics. Cambridge University Press, 1997. ISBN 978-0-521-63396-3. doi: 10.1017/CBO9780511810633.
- Carsten Wiuf and Chuang Xu. Classification and threshold dynamics of stochastic reaction networks, 2023. URL <https://arxiv.org/abs/2012.07954>. Version 3, 24 January 2023.
- Chuang Xu. On the regularity of reaction systems, 2026. URL <https://arxiv.org/abs/2409.05340>. Version 2, revised 9 May 2026.