Tick-Per-Bit (TPB): A Kinetic Model for Chemical Reaction Speed

---

Abstract for General Readers

Why do some chemical reactions happen quickly while others take forever?

The traditional answer focuses on energy barriers—reactions are slow when molecules must climb a tall energy "hill." This paper proposes a different lens.

Before a reaction completes, molecules undergo constant fluctuations—vibrating, rotating, colliding with neighbors, sampling configurations and snapping back. Most fluctuations lead nowhere. No permanent record is created. We call these *ticks*: explorations that haven't yet committed to an outcome.

Eventually, the reaction commits. A bond breaks irreversibly. A product forms and escapes. The system crosses a threshold from which there's no return—a permanent record now exists. We call this commitment a *bit*, borrowing from information theory.

Here's the key insight: these two kinds of change follow different rules.

The cost of commitment (the bit) is fixed by thermodynamics—a floor that doesn't depend on catalyst, solvent, or pathway. But the efficiency of exploration (the ticks) varies enormously. A catalyst doesn't reduce the commitment cost; it makes ticks more productive. A viscous solvent doesn't change what "completing a reaction" means; it makes ticks weaker and less frequent.

This separation has consequences.

It explains why enzymes are sensitive to viscosity and crowding in ways barrier-focused theories struggle to capture. It explains "bursty" single-molecule kinetics—periods of rapid activity followed by long pauses. It predicts that slowing reactions by weakening ticks shouldn't change the minimum heat dissipated per reaction event.

The paper develops this mathematically, applies it to a concrete enzyme example, and specifies what experimental results would prove it wrong.

The deep question shifts from "how high is the barrier?" to "how efficiently does the system convert reversible exploration into irreversible commitment?"

Technical Abstract

We present the Tick-Per-Bit (TPB) framework as a mathematical model of chemical reaction kinetics grounded in information-theoretic principles. The framework separates two contributions to reaction dynamics: (i) an irreducibility floor of order k_B ln 2 per coarse-grained event decision (reactant retained vs. product established), used as the accounting atom for event-counting kinetics, and (ii) variable tick efficiency characterizing the rate and strength of reversible fluctuations that accumulate toward commitment. The resulting rate law k ≈ λμ (tick frequency × tick strength) explains environment-dependent rate variations—including viscosity effects, molecular crowding, and dynamic disorder—without requiring activation free energy shifts as the primary explanatory variable. We extend the model to two-state enzyme kinetics, derive quantitative predictions for bursty single-molecule turnover statistics, and establish explicit falsification criteria including a primary experimental signature. TPB reframes classical Arrhenius/Eyring kinetics as a special case governing tick statistics while revealing the bit/tick separation as the deeper structural principle.

Table of Contents

Appendices

---

1. Introduction: Two Kinds of Change

For general readers: This section explains the core distinction that makes TPB different from traditional kinetics.

What happens during a chemical reaction?

If you learned chemistry in school, you probably learned about activation energy—the "hill" that reactants must climb before they can become products. This picture, formalized by Arrhenius in 1889 and refined by Eyring in the 1930s, has been enormously successful. It explains why reactions speed up when you heat them, why catalysts work, and how to predict reaction rates from molecular properties.

But this picture leaves something out.

Between the moment a reaction "starts" and the moment it "finishes," the molecules aren't simply climbing a hill. They're undergoing constant, rapid fluctuations—vibrating at frequencies of 10^{13} times per second, colliding with solvent molecules billions of times per second, sampling configurations and immediately abandoning them. Most of these fluctuations accomplish nothing. The system explores, backtracks, explores again.

Occasionally, these fluctuations accumulate in just the right way, and the reaction commits. A bond breaks irreversibly. A product forms and escapes. The system crosses a point of no return.

The two kinds of change

TPB formalizes this distinction:

Reversible fluctuations (ticks) are the constant micro-explorations that don't create permanent records. A molecule vibrates—and vibrates back. A configuration is sampled—and rejected. These are "free" in the sense that the universe doesn't have to remember them. They can be undone without any fundamental cost.

Irreversible commitments (bits) are the threshold-crossings that create distinguishable outcomes. Before: the system could have gone either way. After: the system has definitively become something different, and this difference is recorded in the physical state of the universe.

Why this separation matters

Traditional kinetics focuses almost entirely on the commitment event—specifically, on the energy barrier that must be surmounted to reach the transition state. The fluctuations leading up to this are treated as thermal noise that either succeeds or fails in pushing the system over the barrier.

TPB inverts this emphasis. The commitment (the bit) has a fixed thermodynamic cost that cannot be reduced—it's set by fundamental physics. What varies is the efficiency of the exploration process (the ticks). A catalyst doesn't reduce the cost of commitment; it makes the ticks more effective. Environmental changes like viscosity don't change what it means to complete a reaction; they change how efficiently fluctuations accumulate toward commitment.

This reframing has predictive power. It explains phenomena—like viscosity-dependent rate changes that exceed Arrhenius predictions, or bursty single-molecule kinetics—that are awkward for barrier-focused theories.

The deep question shifts from "how high is the barrier?" to "how efficiently does the system convert reversible exploration into irreversible commitment?"

---

2. The Fixed Cost of Commitment

For general readers: This section explains why there's a minimum "price" for making any irreversible change, and what sets that price.

2.1 What makes a change "irreversible"?

Imagine you have a box with a partition down the middle. On the left side: pure nitrogen. On the right side: pure oxygen. Now remove the partition. The gases mix. You now have air on both sides.

Can you unmix them spontaneously? No. The mixed state is overwhelmingly more probable than the separated state. To restore the original configuration, you'd have to do work—run a separation process, spend energy.

This is irreversibility: the system has moved to a state that won't spontaneously reverse, and this transition has increased the entropy of the universe.

A chemical reaction does something similar. Before the reaction, the system is identifiably in a "reactant" state. After, it's identifiably in a "product" state. This distinction—this recorded difference—is what we mean by an irreversible commitment.

2.2 The Landauer bound: the minimum cost of recording

In 1961, physicist Rolf Landauer proved something remarkable: there is a fundamental minimum energy cost to erasing one bit of information. This cost is:

E_min = k_B T ln 2

where k_B is Boltzmann's constant and T is temperature. At room temperature (300 K), this is about 2.87×10^{-21} joules—a tiny amount, but nonzero.

Landauer was thinking about computers, but his result is far more general. Any process that creates irreversible distinguishability—that records a "this, not that" distinction in the physical state of the universe—must pay at least this cost in entropy increase:

$$\Delta S_{bit} = k_B \ln 2 \approx 0.693\ k_B$$

This is not an approximation or a model assumption. It's a consequence of the second law of thermodynamics.

Technical note for readers familiar with Landauer's original formulation: Landauer's bound strictly applies to erasure—resetting a bit to a known state. TPB applies it to creation of distinguishability. The connection is that erasure and creation are thermodynamically symmetric: creating a recorded distinction in a system previously lacking that distinction is equivalent to erasing the system's prior uncertainty about which state it occupies. Both operations require dissipation of at least $k_B T \ln 2$.

2.3 Applying the bound to chemical reactions

Each completed chemical reaction creates distinguishability: the system transitions from "identifiably reactant" to "identifiably product." This is exactly the kind of irreversible record that the Landauer bound constrains.

Here, "one bit" denotes the minimal irreversible decision that separates "reactant identity retained" from "product identity established" at the observational coarse-graining relevant to kinetics. Finer-grained microstate distinguishability can be multi-bit, but the kinetic event-count is defined by this coarse-grained commitment boundary.

Why S = 1 specifically? The threshold is operationally defined by whatever distinguishability criterion the experimentalist uses to count turnovers—fluorescence switching, product appearance, conformational change detection. TPB normalizes this criterion to $S = 1$ by definition. If a different experimental setup required "more distinguishability" to count an event, it would effectively be counting different (composite) events, each still subject to their own irreducibility floor.

This is not arbitrary—it's the natural normalization. The Landauer bound applies to *any* binary decision boundary. TPB takes the experimentally-defined "reaction happened vs. didn't happen" boundary as its unit. The rate law $k \approx \lambda\mu$ is invariant under rescaling: if you doubled the threshold to $S = 2$ (requiring "two bits" per counted event), you'd halve μ by definition, leaving k unchanged.

This is an important subtlety. We're not claiming that every reaction involves exactly one bit of information in some absolute sense. We're claiming that *whatever* distinguishability threshold defines "a reaction" for counting purposes, that threshold carries an irreducibility floor, and TPB uses this floor as its structural anchor.

2.4 What the bound does and does not claim

The bound is a floor, not a typical value. Real biochemical reactions dissipate 10–100 $k_B T$ per turnover—vastly more than the Landauer minimum. Real reactions are far from the thermodynamic limit.

The bound doesn't depend on pathway. Whether you use a catalyst, change the solvent, or modify the temperature, the minimum cost of the irreversible commitment itself doesn't change. What changes is how much *additional* dissipation occurs due to inefficient tick processes.

The bound is what TPB holds fixed. While traditional kinetics might view dissipation as a byproduct of reaction dynamics, TPB treats the bit cost as the invariant anchor point. Everything else—how fast you get there, how much extra heat you waste—depends on tick efficiency.

TPB does not claim that real turnovers saturate this bound; it uses the bound to formalize the existence of a nonzero irreversibility floor associated with event definition. The bound provides a structural anchor for the theory, not a quantitative prediction of actual dissipation.

2.5 Multi-step reactions

Complex reactions involving multiple bond changes or sequential steps correspond to multiple threshold crossings—multiple bits. Each crossing incurs its own $\Delta S_{bit} = k_B \ln 2$.

The choice of counting reactions in "one-bit" units is an accounting convention that enables clean mathematics. The key physical claim is that *each* irreversible commitment has a fixed minimum cost, regardless of how many commitments a complete reaction mechanism involves.

Caveat on experimental events: Different experimental detection methods (FRET for conformational changes, fluorogenesis for product release, etc.) may define "events" that involve different numbers of sequential commitments. The rate law $k \approx \lambda\mu$ is invariant under rescaling of the commitment threshold, but the dissipation floor prediction assumes each experimentally-counted event corresponds to a single coarse-grained commitment. If an experimental "event" actually comprises multiple sequential irreversible steps, the predicted floor would be correspondingly higher ($n \times k_B \ln 2$ for n commitments). TPB as formulated does not predict how total bit costs distribute across mechanism steps—only that each irreversible step incurs at least $k_B \ln 2$.

---

3. The Tick Process: Reversible Exploration

For general readers: This section describes what's happening at the molecular level before a reaction commits—the constant fluctuations that most of us never think about.

3.1 The molecular reality of "waiting"

When we say a reaction takes one second, what's actually happening during that second?

The reactant molecules aren't sitting frozen, waiting for permission to react. They're in constant, violent motion:

- **Vibrations**: Chemical bonds vibrate at frequencies around 10^{13} Hz—ten trillion oscillations per second. Every bond is constantly stretching and compressing.
- **Rotations**: Molecules tumble and spin, reorienting millions of times per second.
- **Collisions**: In liquid solution, a molecule collides with its neighbors roughly 10^{12} times per second. Each collision transfers momentum and energy.
- **Conformational sampling**: Flexible molecules constantly explore different shapes—folding, unfolding, twisting—sampling configurations and immediately relaxing back.

Most of these fluctuations don't contribute to the reaction. They're explorations that lead nowhere. But occasionally, fluctuations align in just the right way: the right bond stretches at the right moment, energy concentrates in the right mode, the geometry achieves the right configuration—and the system crosses the commitment threshold.

3.2 Ticks as the mathematical model of exploration

TPB models these fluctuations as a *tick process*:

- **Ticks arrive randomly** at an average rate λ (ticks per second). This reflects the stochastic nature of thermal fluctuations.
- **Each tick contributes random progress** $X_i \geq 0$ toward the commitment threshold. Some ticks are productive (large X_i); most accomplish little (small X_i).
- **Progress accumulates** until the threshold is crossed. The total progress after n ticks is $S_n = \sum_{i=1}^{n} X_i$.

S is a dimensionless progress coordinate normalized so that S = 1 corresponds to a completed commitment event. This normalization absorbs the physical "size" of a commitment into the definition of μ, making the threshold universal across different reaction types. When $S_n \geq 1$, the reaction commits.

The key parameters are:

- **λ** = tick arrival rate (how frequently the system "tries")
- **μ** = mean tick strength (how much progress a typical try achieves)
- **σ^2** = variance in tick strength (how variable the tries are)

The distribution of X_i encodes mechanism-specific microphysics (vibrational gating, conformational alignment, solvent reorganization), while TPB focuses on the coarse statistics (λ, μ, σ^2) relevant to event timing. This makes TPB an effective theory that abstracts over microscopic details.

3.3 What determines tick parameters?

This is where environment enters the picture.

Tick rate λ depends on:

- Temperature (faster thermal motion → more frequent fluctuations)
- Molecular flexibility (rigid molecules explore more slowly)
- Solvent dynamics (viscous solvents slow conformational motion)

Tick strength μ depends on:

- Mode coupling (how well vibrations and fluctuations connect to the reaction coordinate)
- Friction (high friction dissipates fluctuations before they contribute)
- Crowding (molecular crowding restricts fluctuation amplitude)

This is the key insight: changing viscosity, adding crowding agents, or modifying solvent composition can alter λ and μ substantially—without necessarily changing the activation free energy $\Delta G^\ddagger$ by much.

Traditional kinetics would predict that if $\Delta G^\ddagger$ doesn't change, the rate shouldn't change. TPB predicts that rates can change dramatically through tick efficiency, even when equilibrium properties and barrier heights remain approximately constant.

3.4 An analogy: trying to roll a boulder uphill

Imagine you're trying to roll a boulder over a hill. The hill height is fixed (that's like $\Delta G^\ddagger$). But your ability to actually move the boulder depends on many other factors:

- How often do you get to push? (tick rate λ)
- How effective is each push? (tick strength μ)
- Is the ground muddy or firm? (environmental friction)
- Are there obstacles in your way? (crowding)

You might face two different situations with the *same* hill height but very different outcomes:

Situation A: Firm ground, clear path. Your pushes are frequent and effective. The boulder goes over quickly.

Situation B: Muddy ground, obstacles everywhere. Same hill, but your pushes are weak and often wasted. The boulder takes much longer.

TPB says something similar happens in chemistry. The "barrier" (bit cost) is the same, but the "pushing efficiency" (tick process) differs.

---

4. The Commitment Threshold

For general readers: This section explains when all that random exploration finally "counts" as a completed reaction.

4.1 Crossing the threshold

The reaction completes when accumulated tick progress reaches the commitment boundary:

$S_n \geq 1$

Think of this as filling a bucket one random splash at a time. Each tick adds some water (or sometimes almost none). When the bucket reaches the fill line, the reaction is "done."

The threshold $S = 1$ represents one bit of irreversible commitment—the minimum distinguishable outcome that separates "reaction happened" from "reaction didn't happen."

4.2 Reaction time as first-passage

The reaction time τ is the moment when S_n first crosses 1. In mathematical terms, this is a "first-passage time" of a "compound Poisson process."

This framing connects TPB to a rich literature in probability theory and stochastic processes. First-passage problems appear throughout physics, biology, and finance—anywhere you're asking "how long until a random process first reaches a threshold?"

4.3 The overshoot issue

A technical note for experts: when S_n crosses 1, it typically overshoots slightly. The exact distribution of reaction times depends on this overshoot, which in turn depends on the distribution of tick increments X_i.

Under a small-overshoot / light-tail assumption for X_i, the mean tick count scales as $1/\mu$; more generally $E[n]$ depends weakly on the increment distribution through overshoot corrections.

For most practical purposes—and certainly for the qualitative predictions TPB makes—this correction is minor. The core scaling $k \approx \lambda\mu$ remains robust.

When do higher moments matter? For heavy-tailed X_i distributions or when μ approaches 1 (each tick nearly completes a commitment), overshoot corrections can become significant. In these regimes, the full increment distribution—not just (λ, μ, σ^2)—affects quantitative predictions. TPB as presented is most accurate when ticks are numerous and individually small ($\mu \ll 1$).

---

5. The Core Rate Law

For general readers: This section derives the central prediction of TPB—the equation that says what controls reaction speed.

5.1 A simple derivation

Here's the intuitive argument:

Step 1: Each tick contributes, on average, μ units of progress toward a threshold of 1.

Step 2: Therefore, you need approximately $1/\mu$ ticks to reach the threshold:

$\langle n \rangle \approx 1/\mu$

Step 3: Ticks arrive at rate λ per second. So the average time to accumulate $1/\mu$ ticks is:

$\langle \tau \rangle \approx (1/\mu) \times (1/\lambda) = 1/(\lambda\mu)$

Step 4: The reaction rate k is one over the average reaction time:

$k \approx \lambda\mu$

This is the TPB rate law. Note that k here is the single-molecule event hazard—the turnover rate for one molecule at one commitment boundary. Mapping to bulk (ensemble) rate constants introduces concentration factors and mechanism order, as usual in kinetics.

5.2 What the rate law means

The rate law $k \approx \lambda\mu$ separates reaction speed into two factors:

Factor	Physical meaning	What affects it
λ	How often the system "tries"	Temperature, flexibility, solvent dynamics
μ	How effective each try is	Mode coupling, friction, crowding

Separately, the bit cost $k_B \ln 2$ sets the thermodynamic floor—but it doesn't appear in the rate equation because it's the same for all reactions. It's the invariant, not the variable.

5.3 The slogan

Bits are fixed. Ticks vary.

The minimum irreversibility cost per reaction is set by physics and cannot be engineered away. But the rate at which reactions complete—how quickly the system accumulates ticks toward commitment—is highly tunable through environmental conditions, catalysis, and molecular design.

---

6. Relationship to Classical Kinetics

For general readers: This section explains how TPB connects to Arrhenius and Eyring—the theories you might have learned in chemistry class—and when they agree or disagree.

6.1 The Arrhenius equation

In 1889, Svante Arrhenius proposed that reaction rates follow:

$$k = A \exp(-E_a / k_B T)$$

where E_a is the "activation energy" and A is a "pre-exponential factor." The exponential term captures the intuition that higher barriers mean slower reactions, and higher temperatures mean faster reactions.

Transition state theory (Eyring, 1935) refined this by connecting E_a to a free energy barrier $\Delta G^‡$ and giving a theoretical interpretation of A.

This framework has been enormously successful. It explains the temperature dependence of reaction rates, predicts how catalysts work, and provides a conceptual picture (the "energy landscape") that guides intuition.

6.2 How TPB relates to Arrhenius

TPB does not reject Arrhenius—it reinterprets it.

The activation barrier shapes tick statistics. When $\Delta G^‡$ is high:

- Strong ticks are rare (the system rarely samples configurations near the transition state)
- The effective tick strength μ is low
- Therefore, the rate $k = \lambda\mu$ is low

When tick statistics are dominated by thermal barrier crossing—when environmental coupling is strong and uniform—the product $\lambda\mu$ naturally acquires Arrhenius-like temperature dependence:

$$\lambda\mu \propto \exp(-\Delta G^‡ / k_B T)$$

Arrhenius kinetics emerges as a special case of TPB: the case where tick efficiency is entirely controlled by thermal access to the transition state.

6.3 When Arrhenius is not enough

TPB predicts deviations from Arrhenius behavior when tick efficiency is affected by factors *other than* barrier height:

Viscosity effects: High solvent viscosity slows conformational dynamics (reducing λ) and dampens fluctuation effectiveness (reducing μ)—even when measured barrier proxies change only weakly.

Molecular crowding: Crowded cellular environments restrict fluctuation amplitude and alter solvent dynamics—effects that don't simply map onto barrier changes.

Dynamic disorder: When enzymes switch between internal states with different tick statistics (see Section 7), the resulting kinetics can't be captured by a single barrier height.

In these cases, rates can change substantially even when measured barrier changes are insufficient to explain the observed slowdown. This is the TPB signature.

6.4 TPB and Kramers theory

Kramers (1940) already recognized that reaction rates in solution depend on solvent friction, not just barrier height. In the high-friction limit, Kramers predicted rates proportional to 1/η (inverse viscosity).

TPB is compatible with Kramers—in fact, Kramers emerges as a special case:

Framework	Focus	Key quantity	Primary limitation
Arrhenius/Eyring	Barrier crossing	ΔG‡	Silent on dynamical coupling
Kramers	Diffusive dynamics	Friction η	Single-state; no dissipation constraint
TPB	Bit/tick separation	Tick efficiency λμ	Requires single-molecule data to test fully

In the single-state, diffusive-barrier regime, TPB parameters map onto Kramers quantities: λ relates to attempt frequency, μ relates to transmission coefficient.

What does TPB add beyond Kramers?

1. **The bit-cost anchor**: Kramers predicts a rate; TPB separates rate from irreversibility cost and claims the latter is invariant. This generates the dissipation predictions in Section 9.
2. **Multi-state generalization**: Kramers doesn't naturally handle conformational switching between states with different friction coupling. TPB's tick-throughput formulation (Section 7) extends cleanly to n-state systems with arbitrary switching dynamics.
3. **Conceptual inversion**: Kramers asks "how does friction modify barrier-crossing dynamics?" TPB asks "how efficiently does reversible exploration convert to irreversible

commitment?" This reframing suggests different experimental strategies and connects to information-theoretic bounds.

TPB is not competing with Kramers; it subsumes Kramers as the single-state diffusive limit while adding structure that Kramers alone doesn't provide.

---

7. Two-State Enzyme Extension

For general readers: This section models what happens when an enzyme isn't always in the same "mood"—sometimes it works well, sometimes it doesn't—and shows how this creates distinctive patterns in single-molecule experiments.

7.1 Enzymes aren't machines (exactly)

When we think about enzymes, we often imagine them as tiny machines—each one doing the same thing at the same rate, churning out products like a factory.

Single-molecule experiments reveal a more complex picture. When you watch one individual enzyme (using techniques like fluorescence microscopy), you see something surprising: the same enzyme, in the same solution, doesn't turn over at a constant rate. It goes through periods of rapid activity, then long pauses, then activity again.

This "dynamic disorder" is not experimental noise. It's a real feature of how enzymes work.

7.2 The TPB explanation: state-dependent ticks

TPB explains dynamic disorder through state-dependent tick statistics. The enzyme switches between internal states—different conformations, different dynamic modes—that have different tick efficiencies.

State A (strong ticks): The enzyme is in a "productive" conformation. Fluctuations couple efficiently to the reaction coordinate. Tick rate λ_A is high, tick strength μ_A is high.

State B (weak ticks): The enzyme is in an "unproductive" conformation. Fluctuations are dampened or poorly coupled. Tick rate λ_B is low, tick strength μ_B is low.

The enzyme switches between states:

- A → B with rate α (leaving the productive state)
- B → A with rate β (entering the productive state)

7.3 Effective rate calculation

If the enzyme switches much faster than individual turnovers, it simply averages over states. If it switches much slower, you see distinct periods of fast and slow activity.

The stationary probability of being in each state:

$\pi_A = \beta / (\alpha + \beta)$ $\pi_B = \alpha / (\alpha + \beta)$

The effective mean turnover rate:

$k_{eff} \approx \pi_A \lambda_A \mu_A + \pi_B \lambda_B \mu_B$

7.4 Why this creates bursty kinetics

When the enzyme is in state A, turnovers happen rapidly (rate $\approx \lambda_A \mu_A$). When it's in state B, turnovers are slow (rate $\approx \lambda_B \mu_B$). If state A is much more productive but less common, you get:

- Long idle periods (stuck in state B)
- Bursts of rapid turnovers (when the enzyme enters state A)

This creates non-Poisson statistics. The waiting time between turnovers isn't exponentially distributed—it has a heavier tail, reflecting the possibility of getting "stuck" in the slow state.

7.5 What single-molecule experiments should show

TPB predicts specific, measurable signatures:

- **Heavy-tailed waiting time distributions**: More long waits than a simple exponential would predict
- **Autocorrelation in waiting times**: If one wait is long, the next wait is more likely to be long (you're probably stuck in state B)
- **Characteristic timescales**: The autocorrelation should decay with timescales related to $1/\alpha$ and $1/\beta$

These predictions are testable with current single-molecule techniques.

---

8. Saturation and Tick Bottlenecks

For general readers: This section explains why reactions can slow down for reasons that have nothing to do with energy barriers—and how TPB predicts this.

8.1 The environment as tick supplier

The thermal environment—surrounding solvent molecules, thermal radiation, molecular vibrations—supplies the energy and motion that drive ticks. But this supply isn't unlimited. Environmental coupling can become a bottleneck.

High viscosity: In a viscous solvent, conformational motion is sluggish. The molecule can't explore configurations as rapidly. Tick rate λ drops.

Molecular crowding: In a crowded environment (like the inside of a cell), fluctuation amplitudes are restricted. Neighboring molecules get in the way. Tick strength μ drops.

Poor mode coupling: If the relevant vibrational modes don't connect well to the reaction coordinate, fluctuations dissipate before contributing useful progress. Tick strength μ drops.

8.2 Rate suppression beyond Arrhenius

Here's the key prediction: these environmental effects can suppress reaction rates *even when measured ΔG‡ proxies remain approximately unchanged*.

If you measure the equilibrium constant of a reaction in different solvents and find it's the same (implying similar ΔG), traditional kinetics would predict similar rates. But if one solvent is much more viscous, TPB predicts a slower rate—because tick efficiency is lower.

More precisely: observed rate changes may substantially exceed what barrier shifts alone would predict. TPB explains the excess through tick-efficiency degradation.

8.3 Kramers-like scaling

In the high-friction (overdamped) limit, TPB predicts:

$\lambda \propto 1/\eta$ (tick rate inversely proportional to η) ‖ ‖ $\mu \propto 1/\eta^\alpha$ (tick strength degrades with exponent α)

This connects to Kramers' classic result that diffusive barrier-crossing rates scale as $1/\eta$. But TPB frames this as a tick-efficiency effect rather than a modification of barrier-crossing dynamics.

8.4 Predictions that distinguish TPB from pure barrier theories

1. **Stronger-than-Arrhenius viscosity effects**: Rate suppression at high viscosity should exceed what ΔG‡ shifts predict
2. **Crowding effects orthogonal to barrier effects**: Molecular crowding should affect rates through tick efficiency, partially independently of any barrier changes
3. **Environmental sensitivity of optimized enzymes**: Enzymes that have evolved for maximum speed should show strong dependence on tick-related parameters, because they've already minimized barrier-related delays

9. Thermodynamic Predictions

For general readers: This section connects reaction speed to heat dissipation—how much energy is "wasted" as heat when reactions occur.

9.1 Two kinds of dissipation

TPB distinguishes two dissipation measures that traditional kinetics conflates:

Dissipation per turnover: The heat released each time one reaction event completes. TPB says this has a fixed minimum:

$Q_{\text{per turnover}} \geq k_B T \ln 2 \approx 2.87 \times 10^{-21}$ J at 300 K

This is the irreversible commitment cost—the price of creating one bit of distinguishability.

Dissipation rate: The total heat released per unit time. This scales with how many reactions happen:

$\dot{Q} \geq k \cdot k_B T \ln 2$

Fast reactions dissipate more heat per second, simply because more commitments are happening.

9.2 The TPB prediction about efficiency

Here's a testable prediction: if you slow down a reaction by weakening ticks (increasing viscosity, adding crowding), the dissipation *per turnover* should stay constant or *increase*—not decrease.

Why? The bit cost is fixed. Weakening ticks means more fluctuations are wasted—the system does more useless exploration before each successful commitment. This wasted exploration dissipates energy too.

So tick-weakening should:

- Decrease reaction rate (fewer commitments per second)
- Keep constant or increase dissipation per commitment (same bit cost, more wasted fluctuations)

This is opposite to what you might naively expect. Slower reactions aren't "gentler"—they're *less efficient*.

Experimental status: This prediction is currently untested at the single-molecule level. Measuring dissipation per individual turnover requires calorimetry with single-event resolution—a capability that doesn't yet exist. What *has* been measured is ensemble-average dissipation, which TPB predicts should scale as k × (bit cost + tick waste). Single-molecule calorimetry represents a frontier experimental challenge; successful measurement would provide a strong test of TPB's central claim.

Indirect proxy: Ensemble isothermal calorimetry (ITC) combined with independent rate measurements offers a feasible test. If heat flow $\dot{Q}$ and turnover rate k are measured separately across viscosity conditions, the ratio $\dot{Q}/k$ gives average dissipation per turnover. TPB predicts this ratio should remain constant or increase as viscosity increases; a systematic decrease would weaken the framework. This experiment is achievable with current techniques.

9.3 Efficiency measure

We can define tick efficiency as:

$\eta_{tick} = (k_B T \ln 2) / Q_{actual}$ per turnover

When η_{tick} is low (most reactions), the system wastes lots of energy on unproductive fluctuations. When η_{tick} approaches 1, the system operates near the Landauer limit—nearly every fluctuation contributes usefully to commitment.

Highly optimized molecular machines (like ATP synthase) may approach higher tick efficiencies, though even they operate well above the thermodynamic minimum.

---

10. Continuous Limit

For general readers: This section shows how TPB connects to standard mathematical physics, specifically the theory of random walks and diffusion.

10.1 From ticks to continuous motion

So far we've treated ticks as discrete events—individual fluctuations that arrive one at a time. But when ticks are very frequent (λ very large), the process looks increasingly continuous, like smooth diffusion with drift.

In the limit $\lambda \to \infty$ (with $\lambda\mu$ and $\lambda\sigma^2$ held constant), the progress variable S evolves according to:

$dS = v\, dt + \sqrt{(2D)}\, dW$

where:

- $v = \lambda\mu$ is the drift velocity (systematic progress toward threshold)
- $D = \lambda\sigma^2/2$ is the diffusion coefficient (random spreading)
- dW represents Brownian noise

This is the standard Langevin equation for a diffusing particle with drift—a workhorse equation in physics, chemistry, and biology.

10.2 First-passage to an absorbing boundary

In this continuous picture, the reaction time τ is the first moment when the diffusing "progress particle" reaches $S = 1$, starting from $S = 0$.

This connects TPB to the extensive literature on first-passage problems. Solutions exist for various boundary conditions, drift-diffusion ratios, and initial conditions.

For pure drift (negligible diffusion):

$$\langle\tau\rangle = 1/v = 1/(\lambda\mu)$$

recovering the core TPB rate law.

10.3 The bit/tick separation survives the limit

The continuous limit preserves TPB's essential structure: the boundary location ($S = 1$) is fixed by irreversibility requirements, while the drift and diffusion coefficients (v and D) are determined by tick statistics and hence by environmental conditions.

The bit is still the anchor. The ticks are still the variable.

---

11. Worked Example: Two-State Enzyme Turnover

For general readers: This section applies everything we've developed to a concrete example with actual numbers—showing how TPB makes quantitative predictions that can be compared to experiments.

11.1 The setup

Let's model a real situation: an enzyme that catalyzes a biochemical reaction, observed one molecule at a time.

We'll use TPB to predict:

1. The average turnover rate

2. The pattern of bursty activity
3. What happens when we increase viscosity

...while confirming that the irreversibility cost per turnover stays fixed.

11.2 Parameters for baseline conditions

Our enzyme switches between two conformational states:

State	Description	Tick Rate λ	Tick Strength μ	Throughput $r = \lambda\mu$
A	Productive conformation	2000 s^{-1}	0.020	40 s^{-1}
B	Unproductive conformation	500 s^{-1}	0.002	1 s^{-1}

The enzyme switches between states:

- A → B with rate $\alpha = 0.5\ s^{-1}$ (leaves productive state every ~2 seconds on average)
- B → A with rate $\beta = 0.1\ s^{-1}$ (enters productive state every ~10 seconds on average)

These parameters are chosen to be biologically plausible—similar to values inferred from single-molecule studies of real enzymes.

11.3 Calculation: effective turnover rate

Step 1: State probabilities

How much time does the enzyme spend in each state?

$\pi_A = \beta / (\alpha + \beta) = 0.1 / (0.5 + 0.1) = 1/6 \approx 0.167$ (17% in state A)

$\pi_B = \alpha / (\alpha + \beta) = 0.5 / 0.6 = 5/6 \approx 0.833$ (83% in state B)

The enzyme spends most of its time in the unproductive state!

Step 2: Effective rate

$k_{eff} \approx \pi_A r_A + \pi_B r_B$ $k_{eff} \approx (0.167)(40) + (0.833)(1)$ $k_{eff} \approx 6.68 + 0.83$

$k_{eff} \approx 7.5\ s^{-1}$

Step 3: Interpretation

Mean turnover time: $\tau \approx 1/k_{eff} \approx 0.133$ s (133 milliseconds per turnover)

Despite spending 83% of its time in the slow state, the enzyme achieves 7.5 turnovers per second. The productive state, though rarely occupied, contributes disproportionately because its throughput is 40× higher.

This is a key insight: **rare but efficient states can dominate kinetics**.

11.4 Bursty behavior in single-molecule traces

What would a single-molecule experiment show?

In state A: Expected time between turnovers ≈ $1/r\_A$ = 0.025 s (25 ms). Turnovers come rapidly—a burst of activity.

In state B: Expected time between turnovers ≈ $1/r\_B$ = 1 s. Long pauses between turnovers.

State switching: The enzyme stays in A for about $1/\alpha = 2$ s before switching to B. It stays in B for about $1/\beta = 10$ s before switching back to A.

What you'd see: Long periods (~10 s) of slow, sparse turnovers (state B), punctuated by shorter periods (~2 s) of rapid bursts (state A).

The waiting time distribution would be heavy-tailed: most waits are short (turnovers during state A), but occasional very long waits occur (stuck in state B).

Successive waiting times would be correlated: a long wait suggests you're in state B, and the next wait is likely long too.

11.5 Effect of increased viscosity

Now let's increase viscosity (add glycerol to the buffer, for instance). This weakens ticks but shouldn't change the fundamental thermodynamics.

High-viscosity parameters:

State	Tick Rate λ	Tick Strength μ	Throughput r = λμ
A	800 s^{-1}	0.015	12 s^{-1}
B	200 s^{-1}	0.001	0.2 s^{-1}

Switching rates stay the same ($\alpha = 0.5\ s^{-1}$, $\beta = 0.1\ s^{-1}$)—we're assuming the conformational switching is governed by internal protein dynamics that viscosity affects less than the catalytic fluctuations.

Important caveat: This assumption (viscosity-independent switching) is a simplification appropriate for some systems but not universal. Large-amplitude conformational changes—domain motions, hinge-bending, subunit rearrangements—can themselves be viscosity-dependent. In such systems, both tick parameters *and* switching rates would respond to viscosity, creating richer phenomenology.

Does TPB still make distinguishing predictions when switching is also viscosity-dependent? Yes: even when $\alpha(\eta)$ and $\beta(\eta)$ vary alongside $\lambda(\eta)$ and $\mu(\eta)$, TPB predicts the dissipation floor per commitment remains invariant. Kramers theory alone doesn't make this prediction—it constrains rates but not per-event thermodynamic costs. The bit-cost anchor provides leverage regardless of which parameters viscosity affects.

New effective rate:

$k\_eff \approx (0.167)(12) + (0.833)(0.2)$ $k\_eff \approx 2.00 + 0.17$

$k\_eff \approx 2.2\ s^{-1}$

Result: The reaction slows by a factor of ~3.4 (from 7.5 to 2.2 s^{-1}).

This slowdown occurs despite:

- Same activation barrier (by assumption—we didn't change temperature or substrate)
- Same irreversibility threshold (1 bit)
- Same conformational switching dynamics

This is the TPB signature: environment modifies speed through tick efficiency, not through changing what it means to complete the reaction.

11.6 The invariant: dissipation per turnover

Here's the TPB anchor point. Regardless of rate:

Minimum dissipation per turnover:

$Q\_min = k\_B\ T \ln 2 \approx 2.87 \times 10^{-21}\ J$

This doesn't change between baseline and high-viscosity conditions. The bit cost is fixed.

What does change:

Quantity	Baseline	High Viscosity	Change
k_eff	7.5 s^{-1}	2.2 s^{-1}	3.4× slower
Mean turnover time	0.133 s	0.45 s	3.4× longer
Min. Q per turnover	2.87×10^{-21} J	2.87×10^{-21} J	**Unchanged**
Min. dissipation rate	2.2×10^{-20} J/s	0.6×10^{-20} J/s	3.4× lower

In practice, actual dissipation per turnover likely *increases* in high viscosity, because more fluctuations are wasted. The bit cost is the floor; the actual cost includes all the unproductive ticks too.

---

12. Falsification Criteria

For general readers: A scientific theory must be testable. This section specifies exactly what experimental results would prove TPB wrong.

12.1 What makes a theory scientific?

A theory that can't be proven wrong isn't science—it's speculation. Karl Popper's principle of falsifiability demands that scientific theories make predictions that could, in principle, fail.

TPB makes specific predictions. Here's how to test them.

12.2 Primary experimental signature

If viscosity is varied at constant temperature, TPB predicts:

$k(\eta)$ decomposes into $k(\eta) \propto \lambda(\eta)\,\mu(\eta)$ with measurable dynamical slowdown even when equilibrium constants and inferred $\Delta G^\ddagger$ proxies remain approximately unchanged.

The "smoking gun" signature in single-molecule traces:

PRIMARY SIGNATURE: Increased coefficient of variation in waiting times upon tick-weakening, with emergence of long autocorrelation times ($\sim 1/\alpha$, $1/\beta$) that shift with environment

Operational test: Plot $CV(\tau)$ (coefficient of variation of waiting times) and the autocorrelation function $C_\tau(\Delta)$ versus viscosity η. TPB predicts $CV(\tau)$ increases and a slow correlation component emerges (timescale $\approx 1/(\alpha+\beta)$), while equilibrium proxies (ΔG, K_{eq}) remain near-constant.

Quantitative estimate: Using the worked-example parameters (Section 11), a two-state system with $r_A/r_B = 40$ and $\pi_A \approx 0.17$ has baseline $CV(\tau) \approx 1.3$ (compared to $CV = 1$ for a simple Poisson process). Under 3× tick-weakening where r_A drops from 40 to 12 s^{-1} and r_B from 1 to 0.2 s^{-1}, the state contrast r_A/r_B increases from 40 to 60, and $CV(\tau)$ rises to ≈ 1.5–1.7. The precise value depends on switching-rate responses, but the direction is robust: tick-weakening that preserves or increases state contrast should increase $CV(\tau)$ by 15–30%.

12.3 What would weaken TPB

In single-molecule turnover experiments with controlled tick-weakening (varied viscosity, crowding, or solvent relaxation time), TPB is weakened if:

1. **Waiting times remain near-Poisson** with no emergence of burst/idle structure as ticks weaken, AND
2. **Rates track only ΔG‡ / Arrhenius shifts** while showing negligible dependence on dynamical coupling that's independent of barrier height, OR
3. **Inferred dissipation per turnover decreases** as rates decrease (contrary to the fixed-bit floor).

12.4 Strong falsification

TPB would be strongly falsified by:

- Demonstration that rate changes under viscosity/crowding variation can be *entirely* explained by ΔG‡ shifts with no residual dynamical contribution
- Evidence that dissipation per turnover varies *systematically with rate* in the same direction (both decreasing together would violate the fixed-bit claim)
- Single-molecule data showing no correlation structure in turnover times despite conditions that should favor state-switching

12.5 What would support TPB

Conversely, TPB is supported by:

- Rate suppression under tick-weakening that *exceeds* Arrhenius predictions based on measured barrier changes
- Invariant or increased dissipation per turnover even as rate decreases
- Burst/idle patterns in single-molecule traces with timescales matching predicted switching rates
- Crowding effects that are partially orthogonal to barrier-height effects
- Coefficient of variation in waiting times that increases systematically with tick-weakening

---

13. Discussion: What TPB Changes

For general readers: This section steps back to explain the big picture—how TPB changes the way we think about chemical reactions.

13.1 The structural inversion

Traditional kinetics asks: "What barrier must the system surmount?"

TPB asks: "How efficiently does the system convert exploration into commitment?"

This is not just a different question—it's a structural inversion:

	Classical Kinetics	**TPB**
Speed determined by	Barrier height $\Delta G‡$	Tick efficiency $\lambda\mu$
Irreversibility is	A consequence of kinetics	A fixed constraint
Environment affects	The effective barrier	Tick statistics
Fundamental invariant	None specified	Bit cost per commitment

Classical kinetics treats entropy production as a byproduct—something that happens because reactions happen. TPB treats the entropy cost (the bit) as the anchor point, with kinetics being the variable efficiency of reaching that anchor.

13.2 Comparison to competing explanations

When enzymes show viscosity dependence exceeding Arrhenius predictions, practitioners currently invoke several explanations:

Conformational gating: The idea that protein conformational changes, not chemical steps, become rate-limiting. TPB translates this: conformational gating is a form of tick-rate limitation (reduced λ).

Protein friction / internal viscosity: The proposal that proteins have internal friction that adds to solvent friction. TPB translates this: internal friction affects tick strength (μ) through mode-coupling efficiency.

Dynamic disorder / fluctuating enzymes: The observation that single enzymes show rate fluctuations. TPB explains this through state-dependent tick statistics, making quantitative predictions about waiting-time distributions.

Kramers turnover: The transition from energy-diffusion-limited to spatial-diffusion-limited kinetics. TPB identifies this as a transition between tick-frequency-limited and tick-strength-limited regimes.

Does TPB merely relabel these explanations, or does it add predictive content?

The distinction matters. TPB adds the bit-cost anchor, which generates a prediction none of these frameworks make on their own:

DISTINGUISHING PREDICTION: Dissipation per turnover should remain invariant or increase under tick-weakening, regardless of whether the slowdown is attributed to conformational gating, protein friction, Kramers effects, or any other mechanism.

Conformational gating frameworks predict rate changes but are silent on dissipation per event. Protein friction models predict rate-viscosity relationships but don't constrain the thermodynamic cost per turnover. TPB, through the bit-cost anchor, predicts that this cost has a floor that is mechanism-independent.

This is not relabeling—it is a novel constraint that unifies the existing explanations while generating testable consequences they lack.

13.3 Promising experimental systems

TPB predictions could be most cleanly tested in:

Single-molecule fluorogenic enzyme assays: Systems like β-galactosidase with fluorogenic substrates allow direct measurement of turnover waiting times. Varying viscosity while monitoring waiting-time distributions would test the $CV(\tau)$ prediction directly.

F_1-ATPase rotation experiments: The stepping rotation of F_1-ATPase can be tracked at single-molecule resolution. This system shows clear conformational substates and would allow testing of state-dependent tick statistics.

DNA polymerase fidelity measurements: Replication fidelity involves irreversible commitment decisions. The interplay between speed and error rate under varying conditions could test TPB's predictions about tick efficiency and commitment thresholds.

Ribosome translation kinetics: Single-molecule ribosome experiments reveal complex waiting-time distributions. TPB predicts specific relationships between codon-dependent rates and environmental coupling.

13.4 What TPB explains naturally

Several phenomena that seem anomalous from a pure barrier-crossing perspective emerge naturally from TPB:

Viscosity anomalies: Reactions that slow down "too much" when viscosity increases, beyond what barrier models predict. TPB: tick efficiency degradation.

Crowding effects: Rate changes in crowded cellular environments that don't map cleanly onto barrier changes. TPB: restricted fluctuation dynamics.

Dynamic disorder: Bursty single-molecule kinetics with heavy-tailed waiting times and correlated fluctuations. TPB: state-dependent tick statistics.

Catalytic efficiency limits: Why some enzymes seem to have reached a "speed limit" despite ongoing evolutionary pressure. TPB: they've optimized tick efficiency and are approaching fundamental constraints.

13.5 New questions TPB enables

If TPB is correct, it opens new research directions:

- **Tick efficiency optimization**: How do evolved enzymes maximize $\lambda\mu$? What structural features confer high tick efficiency?
- **Cellular energy budgets**: What fraction of cellular energy expenditure reflects tick inefficiency vs. fundamental bit costs?
- **Molecular machine design**: Can synthetic molecular machines be designed to approach the Landauer limit? What's the practical minimum?
- **Crowding as a control mechanism**: Could cells regulate reaction rates by modulating tick efficiency through crowding, independent of substrate or enzyme concentrations?

13.6 Connection to entropy-time frameworks

TPB connects naturally to broader theoretical programs exploring the relationship between entropy, information, and time. The bit/tick separation suggests that irreversibility (entropy production) and dynamics (time evolution) are coupled but distinct: the bit defines *what* must happen thermodynamically, while ticks determine *when* it happens dynamically.

This resonates with frameworks that treat time emergence as fundamentally connected to entropy flow—the "tick" can be understood as a unit of entropic exploration, while the "bit" represents the irreversible record that such exploration eventually creates. TPB operationalizes this connection in a domain (chemical kinetics) where quantitative predictions can be tested.

13.7 Connections to established frameworks

TPB doesn't stand alone—it connects to several established theoretical frameworks:

Stochastic thermodynamics: The bit cost is a special case of thermodynamic bounds on information processing.

Kramers theory: Tick frequency in the diffusive limit connects to Kramers' friction-dependent rate expressions (Section 6.4).

Single-molecule enzymology: Dynamic disorder and fluctuating enzymes are naturally described by state-dependent tick statistics.

Information thermodynamics: The reaction-as-bit-commitment framing connects to Maxwell's demon, Landauer's principle, and the thermodynamics of measurement.

---

14. Conclusion

The Tick-Per-Bit framework separates chemical kinetics into two fundamentally different contributions:

The bit: the irreversible commitment that creates a distinguishable outcome. This has a fixed minimum cost—$k_B \ln 2$ per commitment—set by thermodynamics and independent of pathway, catalyst, or environment.

The ticks: the reversible fluctuations that accumulate toward commitment. These have variable efficiency—determined by environmental coupling, molecular dynamics, and conformational statistics.

This separation:

1. **Explains environment-dependent rate variations** without requiring barrier changes as the primary explanation
2. **Predicts specific patterns** in single-molecule turnover statistics—bursty kinetics, heavy-tailed waiting times, correlated fluctuations
3. **Establishes a thermodynamic floor** for dissipation per reaction event, with excess dissipation attributed to tick inefficiency
4. **Reframes classical Arrhenius kinetics** as a special case where tick statistics are dominated by thermal barrier crossing

The framework is falsifiable: it makes specific predictions about viscosity effects, waiting time statistics, and dissipation scaling that can be tested against experiment.

Most fundamentally, TPB suggests that the deep question about reaction speed is not "how high is the barrier?" but "how efficiently does the system convert reversible exploration into irreversible commitment?"

Appendix A: Symbol Reference

Symbol	Meaning	Units
k_B	Boltzmann constant (1.38×10^{-23} J/K)	J/K
T	Temperature	K
ΔS_{bit}	Entropy increase per bit commitment	J/K
λ	Tick arrival rate	s^{-1}
μ	Mean tick strength	dimensionless
σ^2	Tick strength variance	dimensionless
S_n	Accumulated progress after n ticks	dimensionless

Symbol	Meaning	Units
X_i	Progress increment from tick i	dimensionless
τ	Reaction time (first-passage time)	s
k	Rate constant	s^{-1}
α	Switching rate A → B	s^{-1}
β	Switching rate B → A	s^{-1}
π_A, π_B	Stationary state probabilities	dimensionless
r_s	Tick throughput in state s ($= \lambda_s \mu_s$)	s^{-1}
$\Delta G^\ddagger$	Activation free energy	J
η	Viscosity / friction coefficient	Pa·s or kg/(m·s)
Q	Heat dissipation	J
$\dot{Q}$	Dissipation rate (power)	J/s = W

Appendix B: Key Equations Summary

Bit cost (thermodynamic floor):

$\Delta S_{bit} = k_B \ln 2 \approx 0.693\, k_B$

$Q_{min} = k_B T \ln 2 \approx 2.87 \times 10^{-21}$ J at 300 K

Tick accumulation:

$S_n = \sum_{i=1}^{n} X_i$ (progress after n ticks)

Reaction completes when $S_n \geq 1$

TPB rate law:

$k \approx \lambda\mu$

Two-state extension:

$\pi_A = \beta / (\alpha + \beta)$ $\pi_B = \alpha / (\alpha + \beta)$

$k_{eff} \approx \pi_A \lambda_A \mu_A + \pi_B \lambda_B \mu_B$

Dissipation bounds:

$Q_{per\ turnover} \geq k_B T \ln 2$ (per event)

$\dot{Q} \geq k \cdot k_B T \ln 2$ (per unit time)

Continuous (drift-diffusion) limit:

$dS = v\,dt + \sqrt{(2D)}\,dW$

$v = \lambda\mu$ (drift) $D = \lambda\sigma^2/2$ (diffusion)

Appendix C: TPB as a Minimal Clock Model

This appendix develops a speculative connection between TPB and theories of time emergence. The interpretation is conceptually suggestive but goes beyond the testable kinetics predictions of the main paper. It is included to indicate how TPB might connect to broader theoretical frameworks.

TPB admits an interpretation as a minimal "clock model" in which the passage of time is operationally identified with the accumulation of irreversible commitments.

Bit-time correspondence

Let B(t) denote the number of coarse-grained event decisions (reactant retained vs. product established) recorded up to coordinate time t. Define experienced time:

$d\tau_{exp} \propto dB$

The local "experienced time rate" then scales with the bit-production rate:

$d\tau_{exp}/dt \propto \dot{B}(t)$

In the TPB hazard approximation, $\dot{B} \sim k \sim \lambda\mu$: the frequency and effectiveness of reversible exploration (ticks) determine how quickly irreversible records form.

Time flow as tick efficiency

This creates a direct relationship between dynamical coupling and time flow:

Regime	λμ	Bit rate $\dot{B}$	Time flow
Efficient exploration	High	Fast	Rapid
Suppressed dynamics	Low	Slow	Stalled
Decoupled system	→ 0	→ 0	Frozen

In strongly suppressive environments—under extreme dynamical decoupling or at coarse-grainings where commitment events become unresolvable—$\lambda_{eff}\,\mu_{eff}$ may approach zero, causing the effective bit rate to collapse. Time-as-bit-progression stalls in that description.

(Whether this framework extends to gravitational contexts such as observer-dependent horizons remains an open question beyond the scope of this paper.)

The tick as time's traction point

Microscopic dynamics are time-symmetric: molecular vibrations, collisions, and fluctuations have no preferred direction. Macroscopic time has an arrow: we remember the past, not the future; reactions proceed toward equilibrium.

The tick process bridges these levels. Ticks are individually reversible—each fluctuation could, in principle, undo itself. But their *accumulation* toward commitment is statistically irreversible. The tick is where time-symmetric exploration converts into time-asymmetric record.

Time flows when bits form. Ticks are where the arrow of time gets its traction.

Observer and coarse-graining dependence

The bit-count $B_\Gamma(t)$ depends on the coarse-graining level Γ chosen by the observer. Different observers, using different criteria for "reaction happened," will count different bit rates and therefore experience different time flows for the same underlying process.

This is not a defect but a feature: it makes explicit that "time" in TPB is relational—defined by the rate of distinguishable record-formation relative to a chosen resolution.

Connection to entropy-time frameworks

This interpretation connects TPB to broader theoretical programs (including VERSF) that propose time emergence is fundamentally linked to entropy flow:

- Each bit costs $\Delta S = k_B \ln 2$ in entropy production
- Bit production rate $\dot{B}$ therefore scales with entropy flow rate
- Experienced time τ_{exp} tracks cumulative entropy production at the event-counting level

TPB operationalizes the entropy-time connection in a domain (chemical kinetics) where the relationship can be quantified and tested.